Run on: OM protein - protein search, using sw model November GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd 8, 2002, 09:33:21; Search time 35.3333 Seconds (without alignments) 37.723 Million cell updates/sec

Scoring table: Sequence: Perfect score: BLOSUM62 US-09-657-431-5 75 RNPDGDVGGPWK 12

747574 seqs, 111073796 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

747574

Minimum DB Maximum DB seq seq length: 2000000000 length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database 4: 5: 6: 7: 7: 10: 111: 113: 114: 115: 116: 116: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: *
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT: * A_Geneseq_032802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	75	100.0	12	22	AAB92091	Laminin fragment S
2	75	100.0	12	22	AAB36566	Mammalian kringle
ω	70	93.3	11	18	AAW34297	Kringle 5 peptide
4	70	93.3	11	21	AAB01898	Human plasminogen
G	70	93.3	18	22	AAG67233	Antigenic peptide
6	70	93.3	23	22	AAB83293	Kringle peptide #2
7	70	93.3	23	22	AAB92096	Laminin fragment S
80	70	93.3	23	22	AAB36570	Mammalian kringle
9	70	93.3	24	22	AAB92090	Laminin fragment S
10	70	93.3	24	22	AAB92095	Laminin fragment S
11	70	93.3	24	22	AAB36565	Mammalian kringle

17-MAY-1999; 10-SEP-1999; 15-OCT-1999;

99US-0134406. 99US-0153406. 99US-0159783.

Modifying and attaching therapeutic peptides to albumin prevents

WPI; 2001-112059/12.

Bridon DP,

Ezrin AM,

Milner PG,

Holmes

DL,

Thibaudeau

(CONJ-) CONJUCHEM INC.

443	421	39	37 38	36	ω ω л 4	33	32	31	30	29	28	27	26			23	22	21	20	19	18	17	16	15	14	13	12
70 70 70	70	70 70	70 70	70	70 70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70
ω ω ω	93.3	ωω.	93. 93. 3	ω.	ມ ເມ	w ·	·	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	ω.	93.3	·
791 791 807	791 791	790 791	566 790	476	453	437	380	371	357	271	266	266	266	192	189	104	101	101	101	101	101	98	95	93	91	90	79
21 22 13	21	22 18	20 15	13	20	19	13	μ ω	20	21	22	22	22	21	21	21	21	21	21	18	18	21	21	21	21	21	18
AAY50867 AAG67223 AAR20013	AAB01887 AAX99589	AAB36562 AAW34285	AAY02100 AAR60519	AAR22503	AAW95051 AAR99499	AAW51457	AAR22504	AAR22502	AAY25408	AAB08407	AAU32136	AAU32129	AAU32126	AAB01919	AAB01918	AAB01915	AAB01912	AAB01892	AAB01890	AAW34288	AAW34286	AAB01916	AAB01913	AAB01917	AAY58868	AAB01914	AAW19256
Human plasminogen Amino acid sequenc PA mutant Plg 1-54		Mammalian kringle Human plasminogen.	A multifunctional Human 'Glu' plasmi	[GARSYQ]-[Plasmino	Amino acid sequenc	Human plasminogen	[GARSYQ]-[Plasmino	[GARSYQ]-[Plasmino	Human tissue facto	A human angiogenes	Novel human secret	Novel human secret	Novel human secret	Human plasminogen	Human plasminogen	Human plasminogen	Human plasminogen	Rhesus monkey plas	Human plasminogen	Monkey kringle 5 p	Human kringle 5 pe	Human plasminogen					

ALIGNMENTS

AAB92091 RESULT 1 blood component; modification; succinimidyl; maleimido grohydroxyl; thiol; hormone; growth factor; neurotransmitter Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; AAB92091 standard; Peptide; 12 Synthetic Laminin fragment SEQ ID NO:1267. AAB92091; 17-MAY-2000; 2000WO-US13576 23-NOV-2000 WO200069900-A2. Homo sapiens. 22-JUN-2001 (first entry) A

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В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia; haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                     New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                        Bridon DP, Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                 17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached the aless therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth the active and account activities the statement of the statem
                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2000; 2000WO-IB00763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalian kringle 5 peptide SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Pred. No.
                                                                                                                                                                                                     Thibaudeau K,
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                                                                                                                                                                                                  Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 12;
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    Davidson DJ,
                                                                                                                                                                                         03-MAY-1996;
                                                                                                                                                                                                                                    03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
psorlasis; arthritis; macular degeneration; diabettic retinopathy;
autoimmune disease; ocular disease; capillary proliferation; therapy;
                                                                                               (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                         05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1998 (first entry)
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nes 12; Conserv
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    Gubbins EJ,
                                                                                                                                                                                    97US-0832087
96US-0643219
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Pred. No. 0.00069;
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RESULT 4
AABO1898
ID AABO
XX AABO1898
AC AABC
XX DT 18-:
XX Pla
DE Hum
XX Pla
KW An:
KW An:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangionas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is synthetic a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 43; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-558670/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
          03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human plasminogen kringle 5 peptide fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB01898 standard; peptide; 11 AA.
                                                                                                          05-MAY-1997;
                                                                                                                                                                        02-MAY-2000
                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
          96US-0643219
97US-0832087
                                                                                                          97US-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
0.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                  (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Column 36; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB
Sequence
                                                  exemplifications of the invention.
                                                                                 plasminogen kringle 5-derived peptides synthesised and used in
  11
  AA;
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Query Match Best Local : Matches Local Similarity 1 RNPDGDVGGPW RNPDGDVGGPW 11 Conservative 93.3%; Score 70; DB 21; 100.0%; Pred. No. 0.003; 0; Mismatches 0 Indels 0; 0;

Length 11;

Д Qγ

RESULT 5 Antigenic peptide fragment of human angiostatin. 13-NOV-2001 (first entry) AAG67233 standard; peptide; 18

angiogenic disease; neoplastic disease; connective tissue disorder; rheumatoid arthritis; atherosclerosis; ocular angiogenic disease; diabetic retinopathy; corneal graft rejection; cardiovascular disease; 08-FEB-2000; 2000US-0500397 08-FEB-2001; 2001WO-US04021. Homo sapiens. chronic inflammation; autoimmunity. cerebral vascular disease; diabetes; immune disorder; Angiostatin; plasminogen; sulfydryl donor; angiogenesis; tumour; 16-AUG-2001.

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RESULT 6
AAB83293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method for generating angiostatin in CC vitro. The method comprises contacting plasminogen with a sulfydryl CC donor, or culturing cells capable of producing plasminogen activator CC in conditioned culture medium (CCM) and contacting the CCM with CCC plasminogen. Angiostatin produced by method of the invention is useful CC for treating animals with angiogenesis disease. It is useful for CCC treating an angiogenic disease such as neoplastic diseases (e.g. tumours CCC and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic CCC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis CCC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis CCC cretinopathy, corneal graft rejection, etc), cardiovascular diseases, CCC cerebral vascular diseases, diabetes-associated diseases and immune CCC disorders (e.g. chronic inflammation and autoimmunity). The present cCC sequence represents an antigenic peptide derived from human angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                           Pulmonary delivery of therapeutic agents which are capable of forming
                                                                                                                                                                                                                                                                                                                              Pulmonary delivery; bioconjugation; pulmonary fluid protein; opioid; systemic drug delivery; antihistamine; anti-angina; anti-hypertensive; anti-arrhythmic; anti-depressant; bronchodilator; anti-inflammatory; anti-thyroid deficiency; Kringle.
   prooq
               covalent bonds with amino, hydroxyl or thiol
                                                                   WPI;
                                                                                                  Ezrin AM,
                                                                                                                                                                                                                                                                   WO200117568-A2
                                                                                                                                   (CONJ-) CONJUCHEM INC.
                                                                                                                                                                    07-SEP-1999;
                                                                                                                                                                                                   07-SEP-2000; 2000WO-IB01429
                                                                                                                                                                                                                                       15-MAR-2001
                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                    Kringle peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB83293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB83293 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing angiostatin for treating angiogenic diseases involves contacting plasminogen with plasminogen activator and sulfhydryl donor contacting plasminogen with plasmin which is contacted with sulfhydryl simultaneously, or producing plasmin which is contacted with sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 47; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-550019/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RNPDGDVGGPW 11
                                                                 2001-354657/37.
components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                Fleser A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                99US-0152681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
                                                                                                Robitaille M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Twardowski P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                             Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
             groups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18
                                                                                               Bridon DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
             on
             pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders.
                                                                                                                                                                                                                                                                                                                                                  17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic agent and a reactive group which reacts with groups on pulmonary or blood components to form a stable covalent bond, where the therapeutic agent may be a peptide. Pulmonary drug delivery is useful as it increases the drug retention-time in the lungs and reduces the risk of extrapulmonary side effects. Modified therapeutic agents of this type may be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic agents, anti-depressants, bronchodilators, opioids or their analogues, anti-inflammatory agents, or anti-thyroid deficiency agents. The present sequence is a kringle peptide.
                                                                                                                                                           Disclosure; Page 611; 733pp; English.
                                                                                                                                                                                                                                                       WPI; 2001-112059/12
                                                                                                                                                                                                          peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB92096;
                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laminin fragment SEQ ID NO:1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB92096 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a modified therapeutic agent comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                      DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                       and attaching therapeutic peptides to albumin pudegradation, useful for increasing length of in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                      Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 137; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%; Score 70;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                    PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                   Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
0.0059;
                                                                                                                                                                                                                                                                                 Thibaudeau
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23;
                                                                                                                                                                                                                     prevents
                                                                                                                                                                                                        vivo
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                                                                                                                                                                                                       activity
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AAB36570
IID AAB3
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AC AAB3
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Mamm
DE WAMM
CAPP
CAPP
KW VASS
KW AASS
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Best Local S
Matches 11
                                  groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and osteopathic activities, and is an angiogenesis inhibitor. (I) are useful for treating angiogenesis in a human, where the derivative is reacted with blood proteins. (I) are also useful for manufacturing a medicament extending the in vivo half-life of a kringle 5 peptide in a patient to provide an anti-angiogenic effect. In particular, a modified kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases in the large molecules decreases
                                                                                                                                                                                                                                                                                               The present invention describes a modified anti-angiogenic peptide comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood components to form stable covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalian kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36570 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-090970/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000; 2000WO-IB00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia
                                                                                                                                                                                                                                                                    bonds. The reactive group is selected from succinimidyl or maleimido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPDGDVGGPW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 AA;
      be used for treating inflammatory disorders (e.g. immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thibaudeau K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                        hydroxyl
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can

bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

growth

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (II) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently

Disclosure; Page 609;

733pp;

English

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AAB92090
ID AABS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-immune inflammation, chronic articular rheumatism or psoriasis), disorders associated with inappropriate or inopportune invasion of vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques or osteoporosis), cancer associated disorders (e.g. solid tumours, solid tumour metastases, angiofibromas, retrolental fibroplasia, haemangiomas, Kasposi's sarcoma or other cancers requiring neovascularisation to
                                                                                                                                                                                                                                                                                      17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          support tumour growth). The peptides are useful for treating these diseases in mammalian or human patients. AAB36562 represents a mammalian kringle 5 protein, and AAB36563 to AAB36577 represent specifically
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protection; endogenous therapeutic peptide; peptidase; conjugation;
blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB92090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB92090 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claimed kringle 5 peptides from the present invention
                                                                                                                                                                            peptidase
                                                                                                                                                                             modifying and attaching therapeutic peptides to albumin peptidase degradation, useful for increasing length of i
                                                                                                                                                                                                                                        Bridon DP,
                                                                                                                                                                                                                                                                                                                                     17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                             23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminin fragment SEQ ID NO:1266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001
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11; Conserv
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                                                                                                                                                                                                                                        Ezrin AM,
                                                                                                                                                                                                                                                                                                                                     2000WO-US13576
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                                                                                                                                                                                                                                                                                     99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%;
                                                                                                                                                                                                                                         Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                         Holmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
0.0059;
                                                                                                                                                                                                                                         DL,
                                                                                                                                                                                                                                          Thibaudeau
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                                                                                                                                                                               in vivo a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity
in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the
                                                                                                                                                                                                                                                                                                  Disclosure; Page 611; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                     peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                   and attaching therapeutic peptides to albumin prevents degradation, useful for increasing length of in vivo \boldsymbol{a}\cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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99US-0159783
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                   for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                          PG,
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0.0062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                              peptide can be used for treating inflammatory disorders (e.g. immune and non-immune inflammation, chronic articular rheumatism or psoriasis), disorders associated with inappropriate or inopportune invasion of vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques or osteoporosis), or cancer associated disorders (e.g. solid tumours, solid tumour
                                                                                                                                                                                                                                        comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood components to form stable covalent bonds. The reactive group is selected from succinimityl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and
                                                                                                                                                                with blood proteins. (I) are also useful for manufacturing a medicament extending the in vivo half-life of a kringle 5 peptide in a patient to
                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis,
                metastases, angiofibromas, retrolental fibroplasia, haemangiomas
                                                                                                                                                    provide an anti-angiogenic effect.
                                                                                                                                                                                                          osteopathic activities, and is an angiogenesis inhibitor. (I) are useful for treating angiogenesis in a human, where the derivative is reacted
                                                                                                                                                                                                                                                                                                                                            The present invention describes a modified anti-angiogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-090970/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000; 2000WO-IB00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogen inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                        inappropriate invasion of vessels or cancers in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200070665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian kringle 5 peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36565 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemangioma; Kasposi's sarcoma; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RNPDGDVGGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Page 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0134406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thibaudeau K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                    In particular, a modified kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
. 0.0062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beliveau
                                                                                                                                                                                                                                                                                                                                                                                                                          mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                          Ê
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sarcoma or other cancers requiring neovascularisation to

SSSSXX

B 64

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Matches
                                                                                                                                                                                                                                                                                 activity. The protein can be used to treat angiogenesis mediated diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis, telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial angiogenesis, plaque neovascularisation, coronary or cerebral collaterals, arteriovenous malformations, isohemic limb angiogenesis,
Sequence
                                                                               muscular degeneration, peptic ulcer, Helicobacter related disease, fractures, keloids, vasculogenesis, haematopoiesis, ovulation, menstruation, placentation or cat scratch fever, and to stimulate wound healing. The protein and antibodies generated from it can be used to screen for agonists and antagonists or in detection, imaging and
                                                                                                                                                                                                                                                      corneal diseases, rubeosis, neovascular glaucoma, diabetic retinopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is an isolated fragment of the Kringle 5 peptide corresponding to amino acid 462 of the human plasminogen protein which can be used in a novel method to inhibit endothelial cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 8; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen Kringle 5 peptide - which inhibits endothelial cell proliferation, useful to treat angiogenesis mediated diseases and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis; diagnosis; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human plasminogen Kringle 5 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             support tumour growth). The peptides are useful for treating these diseases in mammalian vuman pattents. AAB36562 represents a mammalian kringle 5 protein, and AAB36563 to AAB36577 represent specifically claimed kringle 5 peptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW19256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW19256 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1996;
13-DEC-1995;
                                                                                                                                                                                                                                retrolental fibroplasia, arthritis, diabetic neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Folkman MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and diagnosis
   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0763528
95US-0008519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US20447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
0.0062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Best Local Similarity

93.3%; 100.0%;

Score 70; Pred. No.

DB 18; 0.019;

Length 79;

Query Match Best Local Similarity

93.3%; 100.0%;

Score 70; Pred. No.

DB 21; 0.021;

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AAB01914
ID AAB(
                                        Вb
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                                                                                                                                                                                                                                                  The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoletic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases.
                                                                                        diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01916-B01919 represent fragments of human plasminogen used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarth
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB01914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01914 standard; Protein; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Page -; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human plasminogen kringle 5 (Val454-Ala543).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2000 (first entry)
                                                                         Note: This sequence is not shown in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNPDGDVGGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                     full length human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0643219
97US-0832087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                       (AAB01887) shown
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                                                                           but is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic;
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RESULT 14
RAY58668
ID 8AY586
XX AAY586
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XX DT 08-MA
XX DT 08-MA
XX DT 08-MA
XX PL MUMAN
XX PL MUMAN
XX PL MUMAN
XX PN WO200
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XX Homo
XX T16-JI
XX Homo
XX Hom
RESULT 15
AAB01917
ID AAB01
XX
AC AAB01
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                            anti-angiogenic polypeptide such as a non-catalytic region of human plasminogen. The MBEs interact independently with thermodynamic additivity, with components of the vascular endothelium. (I) provide targeted delivery of the anti-angiogenic polypeptide to cell membranes and sites of active angiogenesis, particularly the vascular endothelium, and therefore increase the local concentration and reduce the risk of adverse effects on normal processes elsewhere in the vasculature. They are used in a claimed method of treatment of primary or secondary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide. The invention relates to new soluble delivatives (1) of anti-angiogenic polypeptides. (I) comprise 2 or more heterologous membrane binding elements (MBES, see AAYS8855-61) with low membrane affinity that are covalently attached to a soluble low membrane affinity that are covalently attached to a soluble
                                          AAB01917 standard; Protein; 93 AA.
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of human plasminogen mature polypeptide. The invention relates to new soluble derivatives (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New soluble derivative of anti-angiogenic polypeptide useful for treatment of primary or secondary cancers, contains covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182406/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasminogen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic; angiogenesis inhibitor; cancer; tumour; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human plasminogen mature polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58868 standard; Protein; 91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 21; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane-binding elements for targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ADPR-) ADPROTECH PLC
                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                    1 RNPDGDVGGPW 11
                                                                                                                                              RNPDGDVGGPW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPW 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0015505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB02292
                                                                                                                                                                                                                                                  93.3%;
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                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                  Score 70;
Pred. No.
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox VF;
                                                                                                                                                                                                                                                  DB 21;
0.021;
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                   Length 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                              Search completed: November Job time: 35.3333 secs
                                                                                                                                              Вþ
                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                             Matches
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webbe (e.g., psoriasis)), blood vessel diseases (e.g., haemangiomas, osler-Webbe (e.g., haemangiomas, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratt disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human plasminogen kringle 5 (Val454-Phe546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Syndrome), diseases caused by excessive or abnormal stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-349573/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000 (first entry)
                                                                                                                                                                                                                   Local Similarity nes 11; Conserv
                                                                                                   1 RNPDGDVGGPW 11
RNPDGDVGGPW 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; kringle domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0643219.
97US-0832087.
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                                                                                                                                                                                                                                                                              93.3%;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                        Score 70;
                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                   0.022;
                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human plasminogen used
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cat scratch
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osler-Webber
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               0;
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2002, 09:34:51



Copyright GenCore version 5.1.3 (c) 1993 - 2002 Compus Compugen Ltd

OM protein protein search, using sw model

November 8, 2002, 09:35:26; (without alignments)

36.034 Million cell updates/sec

Perfect score: US-09-657-431-11

Sequence: RKLYDY 6

Scoring table: Gapop 60.0 , Gapext 60.0 OLIGO

283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB DB seq length: 0
seq length: 2000000000

Post-processing: Listing first 45

summaries

pir1:*
pir2:*
pir3:*
pir4:*

Database :

PIR_71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	. 14	13	12	11	10	9	œ	7	6	5	4	ω	2	1	Result No.
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83.3	ω	ω	ω	ω	ω ·	ω.	ω	ω	ω.	ω	Ψ	ω.	ω.	ω	ω	ω	ω	w ·	83.3	ω	ω.	ω.	Ü	83.3	Ü		100.0	100.0	Query Match
264	248	247	247	234	234	234	234	232	231	215	209	205	190	187	181	177	129	126	112	110	107	107	104	79	72	42	812	810	Length
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A71853	AE0281	JC5032	JU0393	T52100	A84515	AH2875	A97652	AI3304	T02765	A95406	T03894	в82601	E64358	T47984	A64477	S59643	S22688	AE0091	B29654	G70021	в91202	F86048	G81291	D97807	D82937	B42177	PLMS	PLHU	ID
hypothetical prote	two-component regu	karasurin-B - Tric	karasurin - Mongol	MADS-box transcrip	probable MADS-box	()	response regulator	response regulator	glutathione transf	glutathione transf	MADS box protein -	transcription regu	ribosomal protein	hypothetical prote		hypothetical prote	ipgA protein - Shi	probable flagellar	\Box			hypothetical prote	probable periplasm	ankyrin like prote	conserved hypothet	main-cont	plasmin (EC 3.4.21	plasmin (EC 3.4.21	Description

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379	379	376	376	368	336	326	322	307	305	289	289	283	280	266	264
N	N	N	ν	N	Ν	N	Ν	2	N	2	_	N	Ν	N	2
T41633	S55900	E70361	A90206	F82570	D86710	D90241	A70661	A71602	E83852	JC5606	RLTZT	G75002	D71160	S59237	G97170
psi protein – fiss	DNAJ-like protein	chaperone DnaJ - A	histidinol-phospha	DnaJ protein XF233	collagen adhesin [d-3-phosphoglycera	hypothetical prote	rifin PFB0955w - m	D-alanyl-D-alanine	karasurin C - Tric	rRNA N-glycosidase	chemotaxis protein	probable chemotaxi	hypothetical prote	aminoglycoside N3'

ALIGNMENTS

RESULT PLHU

100	
asmin (EC	asmin (EC 3.4.21.7) precursor [validated] - human
Alternate	Alternate names: plasminogen precursor [misnomer]
Contains:	Contains: angiostatin; microplasmin; plasminogen
Species:	Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. J. Biol. Chem. 265, 6104-6111, 1990 A;Title: Characterization of the gene for human plasminogen, a key proenzyme A;Reference number: A35229; MUID:90202879 A;Accession: A35229. A04625;

ín the f

A; Molecule type: DNA

A;Residues: 1-810 <PET>

A;Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026 A;Experimental source: leukocyte; lung fibroblast R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990 A;Title: Definition of the transcription initiation site of human plasminogen gene in A;Reference number: 15242; MUID:91097523

A;Status: translated from GB/EMBL/DDBJ

A; Residues: A;Molecule type: DNA A;Residues: 1-16 <MAL1>

A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. FEBS Lett. 213, 254-260, 1987

A;Title: Molecular cloning and characterization of a full-length cDNA clone for human A;Reference number: A26646; MUID:87162490 A;Accession: A26646

A;Molecule type: mRNA
A;Residues: 1-471, 'D', 'A73-810 <FOR>
A;Residues: 1-471, 'D', 'A73-810 <FOR>
A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A;Experimental source: liver
A;Experimental source: liver
A;Mailnowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a A; Reference number: I45961; MUID: 85023311

A; Accession: 162738 A;Status: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 292-471, 'D', 473-810 <MAL2> A; Cross-references: GB: K02922; NID: g190112; PIDN:AAA60124.1; PID:g387031

A; Accession: 184609

A;Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 367-419 <MAL3>

A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

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R; Wu, T.P.; rurrus, rubmitted to the Brookhaven submitted to the Brookhaven number: A51911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34
A;Reference number: A92458; MUID:8054794
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid bi
A;Contents: April 1, Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.;
Biol. Chem. 271, 29461-29467, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 483-507, 'E', 509-604 <WI3>
A;Residues: 483-507, 'E', 509-604 <WI3>
B;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria,
J. Biol. Chem. 248, 1631-1633, 1973
A;Title: The primary structure of human plasminogen.
A;Reference number: A92125; MUID:73149248
A;Contents: annotation; active site
A;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
S. Millo Chem. 244, 3590-3597, 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites
A;Reference number: A92382; MUID:82213905
A;Contents: annotation; omega-aminocarboxylic acid binding sites
                                                                                           A; Contents: annotation; X-ray crystallography,
                                                                                                                                                                                                                                                                                                                           R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D. Biochemistry 37, 4699-4702, 1998
B;ochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen A;Reference number: A58812; MUID:9548733
A;Contents: annotation
                                                                                                                         A; Reference number:
                                                                                                                                                                                      R; Tulinsky, A.; Wu, T.P
                                                                                                                                                                                                           A; Contents: annotation; X-ray crystallography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferati A;Reference number: A58811; MUID:97067211
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Vali, Z.; Patthy, L.
T. Biol. Chem. 259, 13690-13694, 1984
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A; Residues: 20-50,'Q',51-71,'E',73-85,87-100
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A;Title: Primary structure of the B-chain
A;Reference number: A04627; MUID:77225245
A;Accession: A04627
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A; Molecule type: protein
A; Residues: 20-71, 'E', 73-76 <BRU>
A; Residues: 21-71, 'E', 73-76 <BRU>
Talin 1977
                                                                                                                                                                                                                                            A; Reference number: A51341; PDB:1PK4
                                                                                                                                                                                                                                                                    submitted to the Brookhaven Protein Data Bank, July 1991
                                                                                                                                                                                                                                                                                                      R;Tulinsky, A.; Mulichak, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A04626
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A; Residues: 20-71, 'E', 73-85,87-106, 'D', 108-360, 'E', 362-810 <SOT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S03735; MUID:81212097
A;Accession: S03735
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                                                                                                                      to the Brookhaven Protein Data Bank, ce number: A51488; PDB:2PK4
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                                    Protein Data Bank,
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                                 August 1993
                                                                                       2.25 angstroms,
                                                                                                                                                 July 1991

    1.9 angstroms,

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A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKH
d PIR:FGHUGB).
                                                                          F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                        C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol C;Reywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; h
                                                                                                                                                                                                                                                                                                                                                                          C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibit C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial c C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin.
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Eur. J. Blochem. 221, 927-937, 1994
A;Title: (1)H-MMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157
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F;20-96/Domain: activation peptide #status experimental <APT>
                                                                                                                                                                                                                                               ns the walls of the graafian follicle; also activates the urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                  A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR: ITHUA2)
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Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined
A;Reference number: A58819; MUID:92031502
                                           F;20-810/Product: plasminogen #status experimental <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
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A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803
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A;Title: The refined structure of the epsilon-aminocaproic acid
A;Reference number: A58818; MUID:92031503
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A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Superfamily: plasmin; kringle homology; plasminogen-related protein; hydr
F;1-95/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence **status predicted <SIG>
F;20-812/Product: plasminogen **status predicted <APT>
F;20-96/Domain: activation peptide **status predicted <APT>
F;97-96/Domain: activation peptide **status predicted <APT>
F;97-81/Domain: activation peptide **status predicted <AAT>
F;97-81/Domain: chain A **status predicted <AAT>
F;103-181/Domain: chain A **status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;103-181/Domain: kringle homology <KR3>
F;275-352/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;481-560/Domain: kringle homology <KR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin mediately after dissociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation peptide.

C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403 R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. Eur. J. Blochem. 224, 863-871, 1994 A;Title: Characterization of the murine plasma fibrinolytic system. A;Reference number: S48202; MUID:95010076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eful in treating solid tumors.

(c)Function:

A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vans the walls of the graafian follicle; also activates the urokinase-type plasminogen act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S48202;
A; Accession: S48202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A38514; A; Accession: A38514
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C;Accession: A38514; S48202; S48203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                       F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;582-805/Domain: trypsin homology <TRY>
F;49-7,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 22-27 <LI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 20-25 <LIJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-812 < DEG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Degen, S.J.F.; Bell, 9
Genomics 8, 49-61, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S48203
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Glu-Asn (stromelysin 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.M.; Schaefer, L.A.; Elliott, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Pred. No.
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13;
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RESULT 5 D97807

ankyrin like protein [imported] - Rickettsia conorii (strain Malish 7)

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F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
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A; Accession: D82937
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: sequence inconsistent with the nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:95677, NCBIP:95689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Constantinou-Deltas, C.D.; Gilbert, J.; Bartlett, R.J.; Herbstreith, M.; Roses, A.D Genomics 12, 581-589, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo saplens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
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Вb
                                     δÃ
                                                                                                                                                                                                                              A;Cross-references: GB:AE002107; GB:AF222894; NID:g6899022; PIDN:AAF30485.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-72 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                 A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
                                                                                                                                                                                                                                                                                                                                                                                                       submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: D82937 R; Glass, J.I.; Lefk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D82937
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A; Residues: 1-42 <CON>
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A; Reference number: A42177; MUID:92217982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: B42177
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                                                                                                                                                                    A; Genetic code: SGC3
                                                                                                                                                                                             A;Gene:
                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical UU080 [imported] - Ureaplasma urealyticum
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Best Local
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                                                                                  Matches
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  RKLYD 54
                                                                                  Similarity
5; Conserv
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                                                                                  Conservative
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Pred. No.
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Pred. No.
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                                                                                    Mismatches
                                                                                           DB _ 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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A;Residues: 1-107 <STO>
A;Cross-references: GB:AE005174; NID:g12518480; PIDN:AAG58850.1; GSPDB:GN00145; UWGP:Z51A;Experimental source: Strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                             A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: P86048
                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli (C;Date: 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: F86048 (R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
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                                                                                                                              A; Molecule type: DNA
                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype;Reference number: A81250; MUID:20150912
A;Accession: G81291
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A;Accession: D97807
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C;Date: 30-Sep-2001 *sequence_revision 30-Sep-2001 *text_change 30-Sep-2001
C;Accession: D97807
                                                                                                                                                                                                                                                                                                                                                                                                            nypothetical protein Z5138 [imported] - Escherichia coli (strain 0157:H7, substrain
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A; Residues: 1-104 <PA
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A; Residues: 1-79 < KUR>
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Science 293,
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Query Match
Best Local Similarity
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R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Bero, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Accession: 670021
A;Gene: yusN
C;Superfamily: Bacillus subtilis hypothetical protein yusN
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                  A;Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15275.1; PID:e11843
A;Experimental source: strain 168
                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-110 <K
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A;TitLe: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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DNA Res. 8, 11-22, 2001
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                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-107 <HAY>
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100.0%; Pred. No. 36
tive 0; Mismatches
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100.0%;

Score 5; Pred. No.

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C;Accession: AE0091
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable flagellar protein flis [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;22/Inhibitory site: Lys (trypsin) *status predicted F;73/Inhibitory site: Met (chymotrypsin, elastase) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: B29654

C;Accession: B29654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteinase inhibitor (PSTI type), submandibular - lion
C;Species: Panthera leo (lion)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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ipgA protein - Shigella flexneri virulence plasmid pWR100
C;Species: Shigella flexneri
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: S22688
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                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: flagellar protein flis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
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F;8-42,20-39,28-60,64-93,71-90,79-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: duplication; saliva; serine proteinase inhibitor; submandibular gland F; 6-60/Domain: Kazal proteinase inhibitor homology < KP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: submandibular proteinase inhibitor; Kazal proteinase inhibitor homology
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A; Residues: 1-112 <REI>
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A; Residues: 1-126 < KUR>
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100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No.
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o. 37;
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A64477
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A; Residues: 1-129 <ALL>
    A; Title: Complete genome sequence of the A; Reference number: A64300; MUID: 96337999 A; Accession: A64477
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A; Residues: 1-177 <DE2>
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A; Residues: 1-177 <DEV>
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A; Map position: 1
A; Introns: 76/1
C; Superfamily: Schizosaccharomyces SPAC13C5.06c
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A;Reference number: Z21731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1995 A; Reference number: $58093 A; Accession: $59643
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blai, R; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1038-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
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A;Accession: S22688
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                                                                                                                                             C;Species: Methanococcus jannaschii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: A64477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z50112; PIDN:CAA90457.1; A;Experimental source: strain 972h-; cosmid c13C5
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A;Status: preliminary; translated
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                                                                                                                                                                                                                              L-fuculose-phosphate aldolase homolog - Methanococcus jannaschii
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100.0%; Pred. No.
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Walsh, S.V.
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the methanogenic archaeon, Methanococcus

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R;Choiste, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; submitted to the Protein Sequence Database, February 2000
A;Reference number: 224481
A;Accession: T47984
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-187 <CHO>
A;Cross references: EMBL:AL138642
A;Cross references: Cultivar Columbia; BAC clone F21F14
C;Genetics:
                                                                                                                                                                                                                                                           A;Map position: 3
A;Note: F21F14.90
C;Superfamily: Arabidopsis thaliana hypothetical protein F21F14.90
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T47984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F21F14.90 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #sequence_revision 20-Apr-2000 #c;Accession: T47984
Search completed: November Job time: 17 secs
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                                                                                         13 RKLYD 17
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OM protein - protein search, using sw model

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US-09-657-431-11 6 1 RKLYDY 6

Title:
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Sequence:

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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SUMMARIES

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                                                                                                                                                                   This
            EMBL; J04766; AAA50168.1; PIR; A38514; A38514.
                                                              or send an email to license@isb-sib.ch)
                                                                                                                                   the
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                                                                                                                                                                                                                                                                                                                                                                                                  <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF ANGIOSTATIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.; "Characterization of the cDNA coding for mouse plasminogen localization of the gene to mouse chromosome 17."; Genomics 8:49-61(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P20918;
                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95042728; PubMed=7525077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91184812; PubMed=2081600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A PROTECLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAPFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINGEN ACTIVATOR, COLLAGEMASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND YON WILLEBRAND FACTOR.
                                                                                                                                                                                                ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREEPFOKINASE.

MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN INMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANEOUS: IN THE PRESENCE OF THE INHEBITOR, THE ACTIVATION INVOLVES ONLY CLERVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELL TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

SIMILARITY: CONTAINS 5 KRINGLE DOMÁINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                               European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                               METASTATIC TUMORS IN VIVO.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                   NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conserv
                                                                         non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 17, Created)
(Rel. 17, Last seq
(Rel. 40, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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6.4;
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SMART; SM00040; TTYP_SPc; 1.
PROSITE; PSS00021; KRINGLE_1; 4.
PROSITE; PSS0070; KRINGLE_2; 5.
PROSITE; PSS0070; TRYPSIN_DOW; 1.
PROSITE; PSS0014; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HSE; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; InterPro; IPR000001; HINTERPRO; IPR003014; HINTERPRO; IPR003609; InterPro; IPR001254; InterPro; IPR001254; I
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MGD; MGI:97620;
                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                         remodeling; Blood
                               Similarity 6; Conserv
                                                            758
812
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Trypsin.
|le; 5.
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Kringle.
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                                       100.0%;
                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          coagulation;
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                                                                      SERINE PROTEASE
CHARGE RELAY SY:
CHARGE RELAY SY:
GY SIMILARITY.
BY SIMILARITY.
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KRINGLE
KRINGLE
KRINGLE
KRINGLE
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ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                  PLASMIN SHORT FORM OF CHAIN
                                       Pred. No.
                                               Score
                                                               D34A74A4FC2256F8 CRC64;
                               Mismatches
                                                                                                                                                                                                                                                                         PROTEASE.

RELAY SYSTEM

RELAY SYSTEM
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n; Kringle; Zymogen;
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SIMILARITY).
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mogen; Signal.
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IPSG_PANLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
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01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
SEQUENCE FROM N.A.
STRAIN-M90T / SEROTYPE
                                                                                                                  Shigella flexneri.
Plasmid 210 kb invasion pWR100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00280; KAZAL; 2. PROSITE; PS00282; KAZAL; 2.
                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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HSSP; P05586; 40VO.
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Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPSG_PANLE P08481;
                                                            NCBI_TaxID=623;
                                                                                Shigella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 2 KAZAL-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reisinger P.W.M., Hochstrasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Submandibular gland;
MEDLINE=87299011; PubMed=3304339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The amino-acid sequences of the double-headed
                                                                                                                                                                          pgA protein.
                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                            1 RKLYD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. Chem. Hoppe-Seyler 368:717-726(1987).
FUNCTION: THIS INHIBITOR IS COMPOSED OF TWO HOMOLOGOUS ACTIVELY
                                                                                                                                                                                                                                                                                                                                                                          RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBITS ELASTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
5; Conserv
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IPR002350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor;
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REACTIVE BOND 2 (
BY SIMILARITY (
BY SIMILAR
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                                                                                                  subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                red. No. 16
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submandibular
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entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                  Hypothetical protein; SIGNAL 1 2:
                                                                                                                                                                                                                                                                                                               EMBL; Z50112; CAA90457.1; -
                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972;
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RESULT 6

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MEDLINE=96337999; pubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Zinc; Complete METAL 68 68
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-i- COPACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).

-i- SIMILARIY: BELLONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/1

-i- SUBFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZAE HI1012.
                                               Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                        Methanococcus jannaschii
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                                                                                                                        Bertani I., Coglievina M., Zaccaria P., Klima R., Bruschi C.V.;
"The sequence of an 11.1 kb fragment on the left arm of Saccharomyces cerevisiae chromosome VII reveals six open reading frames including NSP49, KEM1 and four putative new genes.";
Yeast 11:1187-1194(1995).
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Pfam; PF00281; Ribosomal_L5; 1.
Pfam; PF00673; Ribosomal_L5_C; 1.
ProDom; PD001076; Ribosomal_L5; 1.
PROSITE; PS00358; RIBOSOMAL_L5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a linear statement of the statement is not removed.
                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycesace; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-CCT-1996 (Rel. 34, Last ann
Hypothetical 30.5 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gog
use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                    STRAIN=S288C / FY1679; MEDLINE=96109931; PubMed=8619317;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                     YGL174W OR G1642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MJ0469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U67497; AAB98458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                           SIMILARITY: SOME,
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(Rel. 32, Last sequence update)
(Rel. 34, Last annotation update)

rotein in SAE2-KEM1 intergenic region.
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                                                                                                                                                                                                                                                                                                                                 Saccharomycotina; Saccharomycetes;
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Mismatches
                                                                                                             R08D7.1.
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 and for commercial
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Reich C.I.,
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DR PINS;

DR PRINT;

DR PROSIJ

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Best Local
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01-MAR-2002 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA
N-glycosidase) (EC 3.2.22).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA.
-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY. TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizukami H., Iida K., Kondo T., Ogihara Y.;
"Cloning and bacterial expression of a gene encoding ribosome-
inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
kirilowii var. japonica.";
kirilowii var. japonica.";
Biol. Pharm. Bull. 20:711-713(1997).
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EMBL; Z72696; CAA96886.1; -.
SGD; S0003142; YGL174W.
Hypothetical protein.
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                                                     PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92005921; PubMed=1914000;
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
                    SIGNAL
                                    Antiviral;
                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                 between
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                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 24-270
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; P09989; lмRJ.
                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                         Pro; IPR001574; RIP. PF00161; RIP; 1.
                                                                                                                                                                 AB000666; BAA21786.1;
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                 synthesis inhibitor; Hydrolase; Toxin; Signal. 21 POTENTIAL.
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100.0%;
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Pred. No.
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32;
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STRAIN-MAXIMOMICZ;
MEDLINE-91153657; PubMed-1999291;
MEDLINE-9115567; PubMed-1999291;
MEDLINE-9115567; PubMed-1999291;
MEDLINE-9115567; PubMed-1999291;
MEDLINE-9115567; PubMed-1
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ACT_SITE
HMEDLINE-95344383; PubMed=7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
"Studies on crystal structures, active-centre geometry
depurinating mechanism of two ribosome-inactivating pro
                                                                                                                                                                        MEDLINE-94344957; PubMed-800
Zhou F., Fu Z., Chen M., Lir
"Structure of trichosanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MAXIMOWIC2; TISSUE-Tuberous root; MEDLINE-90256789; PubMed-2341399; Collins E.J., Robertus J.D., Lopresti M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MAXIMOWICZ; TISSUE=Leaf;
MEDLINE=90256790; PubMed=2341400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ribosome inactivating protein alpha-trichosanthin precursor
(rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                 Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Tian G.Y., Ni C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
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                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                               application.
                                                                                                                                                                                                                                                                                                                                       "Scientific evaluation of Tian Hua application.":
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Tuberous root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 24-270.
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                                                                                                                                                      Proteins 19:4-13(1994).
                                                                                                                                                                                                                                                                                                     Pure Appl. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 24-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu P., Hwang K., Piatak M.;
"Primary amino acid sequence of alpha-trichosanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and DNA sequence of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                     (-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                          58:789-798(1986).
                                                                                                                                                                                                                            PubMed=8066085;
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289
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100.0%;
                                                                                                                                                                        Lin Y., Pan K.;
hin at 1.88-A resolution.";
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopresti M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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35;
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                                                                                                                                                                                                                                                                                                                                                                                                        Zhang L.Q., Xia
                                                                                                                                                                                                                                                                                                                                                       (THF): history, chemistry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stone K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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proteins.";
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RESULT 11

RRM1_BROWN
ID RWM1_L
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AC Q9VEI
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DT 16-O
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ACT_SITE
                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ribosomal RNA methyltransferase CG5220
(uridine-2'-O-)-methyltransferase).
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                             Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                               CG5220
                                                                                                                                                                                                                                                                                   Q9VEP1;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 RRM1_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
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   Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 RKLYD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RKLYD 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY. TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bhem. J. 309:285-298(1995).
FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN.
CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
INACTIVATES ENGARYOTIC 60S RIBOSOMAL SUBUNITS.
INACTIVATES ENGARYOTIC 60S RIBOSOMAL SUBUNITS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1TCS; 10-JUL-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A36273; A36273.
A36274; A36274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1MRK; 07-FEB-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1MRJ; 07-FEB-95.
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JT0566; JT0566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M34858; AAA34207.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00396; SHIGARICIN.
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non-profit institutions as long as its content
and this statement is not removed. Usage by ar
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   Drosophilidae;
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MISSING (IN REF. 4).
I -> L (IN REF. 4).
V -> VDAGLPRNAVL (IN REF. 4).
KI -> GL (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KI -> GL (IN REF. 4).

K -> S (IN REF. 4).

SWS -> SLML (IN REF. 4).

Q -> T (IN REF. 4).

S -> T (IN REF. 2).

MISSING (IN REF. 4).

T -> M (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIBOSOME-INACTIVATING PROTEIN ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 35
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5CE09BB630575BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                     302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                    Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                                                                                                                                          (EC
                                                                                                                                                                                    2.1.1.-) (rRNA
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davanport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davanport I.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Daviel S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Daviel S., Carrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Menkulov G., Milshia N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menkulov G., Milshia N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menkulov G., Milshia N.V., Mobarry C., Morris J., McShoron D.L.,
RA Menkulov G., Milshia N.V., Mobarry C., Morris J., McShoron D.L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Kang C., Turrer R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Khimsel S.H., Woodage T., Worley K.C., Wu D., Yang S., Zhou Q.A.,
RA Kang G., Chang R., Shou S., Shou S., Zhou S., Zhou 
밁
                                                                                       Matches
                                                                                                                                  Query Match
                                                                                     Best Local Similarity Matches 5; Conser
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                                                                                                                                                                                                                          FlyBase; FBgn0038471; CG52
InterPro; IPR002877; FtsJ.
Pfam; PF01728; FtsJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                               Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                               EMBL; AE003716; AAF55380.1; -.
                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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61
                                          1 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMOCYSTEINE + RRNA CONTAINING 2'-O-METHYLURIDINE. SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RRMJ
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RKLYD
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                                                                                                                                                                               l protein; 302 AA; 3
                                                                                       Conservative
                                                                                                                                                                               n; rRNA processing; Transferase; Methyltransferase
33402 MW; EDFB3BAD445693DA CRC64;
                                                                                                               100.0%;
                                                                                                                                                                                                                                                                            CG5220.
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                                                                                          Mismatches
                                                                                                   DB
. 36;
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                                                                                       0;
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DDL_BACHD
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DNAJ_XYLFA
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Q9KČFO;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)
QD-Ala-D-Ala ligase).
DDL QR DDLA QR BHIG21.
                                                                                                                                                         Chaperone protein dnaJ. DNAJ OR XF2339. Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Fuji F.,
                                                                                                                                                                                                                                                                                                        Q9PB06;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: ATP + D-alanine + D-alanine = ADP + phosphat.
                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
                    SEQUENCE FROM N.A
                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                               DNAJ_XYLFA
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                                                                           CBI_TaxID=2371;
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SIMILARITY: BELONGS TO THE D-ALANINE-D-ALANINE LIGASE FAMILY.
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PF01820; Dala_Dala_ligas; 2.
TE; PS00843; DALA_DALA_LIGASE_1; 1.
TE; PS00844; DALA_DALA_LIGASE_2; FALSE_NEG.
e; Cell wall; Peptidoglycan synthesis; Comp.
NCE 305 AA; 33125 MW; C806D03993D3D081
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Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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RA COUTING L.L., Cristofani M., Dias-Neto E., Docena C., El Dorry H., RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Frach J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Garnier M., Goldman E.E., Laigret F., Lambais M.R., Leite L.C.C., L., Kitajima J.P., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., L., Martins E.G.M., Lopes S.A., Lopes C.R., Machado J.A., RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., RA Machado M.A., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., NA Martins E.A.L., Martins E.M.F., Matsukuma A.Y., RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., RA Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., RA Monn D.H., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., RA de Silve A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr., RA de Soluza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., RA de Soluza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., Park M. Meidanis J., Setubal J.C.; Subako M.H., Ra Aggo M.A., Zatz M., Meidanis J., Setubal J.C.; Statella J.C., Santonic G. f. the Nath Carbon V.J. 1011 fattidica """
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Pfam; PF00684; DnaJ_CXXCXGXG;
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-i- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE DNAJ FAMILY.
-i- SIMILARITY: CONTAINS 1 CR DOMAIN.
-i- SIMILARITY: CONTAINS 1 CR DOMAIN.
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Simpson A.J.G., Reinach F.C., Aryruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C. Arayr J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Countinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
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the European Bioinformatics Institute.
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InterPro; IPR002939; DnaJ_
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RESULT 14
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Chaperone protein dnaJ-2.
DNAJ2 OR AQ 703.
Aquifer acc.
                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                            PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                           Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aguifex menicus".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQUAE
                                                                            Complete
                                                                                     Chaperone;
                                                                                                                                          Pfam; PF01556; DnaJ_C; 1. Pfam; PF00684; DnaJ_CXXCXGXG;
                                                                                                                                                                   InterPro, IPR003095, DnaJ_C.
InterPro, IPR0030939, DnaJ_CXXCXGXG.
InterPro, IPR001305, DnaJ_CXXCXGXG.
InterPro, IPR001623, DnaJ_N.
                                                                                                                                                                                                         HSSP; P08622;
                                                                                                                                                                                                                   EMBL; AE000703; AAC06881.1;
                                                                                                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                       aeolicus
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Bacteria; Aquificales;
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                                                REPEAT
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SIMILARITY: CONTAINS 1 CR DOMAIN.
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SM00271; DnaJ; 1.
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ZINC 2 (B)
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CXXCXGXG
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CXGXG MOTIF.
CXGXG MOTIF.
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C 1 (BY SIMILARITY).
C 2 (BY SIMILARITY).
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SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

STRAIN-ATCC 35092 / DSM 1617 / P2;

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

De Moors A., Erauso G., Fletcher C., Kozera C.J., Medina N., Peng X.

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Boolittle W.F., Duguet M., Gaasterland T.,

Sensen C.W., Van der Oost J.;
                                                                                                                                  Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
-!- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-
(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 35092 / DSM 1617 / P2; MEDLINE=97352708; Pubmed=9209067;
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15-JUL-1998 (Rel. 36, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charlebois R.L., Sensen C.W., Doolittle W.F. "Evolutionary analysis of the hisCGABdFDEHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulfolobus solfataricus. Archaea; Crenarchaeota; Sulfolobales;
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                  -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
-!- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chaeon Sulfolobus solfataricus P2.";
Bacteriol. 179:4429-4432(1997).
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There are no

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:36:17; Search time 25 Seconds (without alignments) 41.519 Million cell updates/sec

Title: US-09-657-431-11
Perfect score: 6
Sequence: 1 RKLYDY 6

Sequence: 1 RKLYDY 6
Scoring table: OLIGO

ing table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database: SPTREMBL_19:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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PF00089; trypsin; s; pR00722; CHYMOTR S; pR000728; KRINGLE ; SM00130; KR; 1 ; SM00120; Tryp_SPc TE; PS00021; KRINGL TE; PS50070; KRINGL TE; PS50070; KRINGL TE; PS50240; TRYPSI	EMBL; AF029692; AAB97887.1; HSSP; P00747; 5HPG. MEROPS; S01.233; InterPro; IPR001314; Chymotrypsin. InterPro; IPR000001; Kringle. InterPro; IPR001254; Trypsin. Pfam; PF00051; Kringle; 1.	Site Mutation is Associated with Deletion of a Single Exon in a Null Allele."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPESTN PAMILY.	A, Hixson J.E.; of the Apolipoprotein (a) Null Phenotype: A Spl	GMENT). (Hamadryas babooroa; Chordata; Craia; Primates; Cat Papio.	04507; FREIDMINNKI; PKI; 334 AA. 04507; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	1

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PLASMINOGEN PRECURSOR.
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SIGNAL
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SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
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Pfam; PF00024; PAN; 1.
Pfam; PF000089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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HSSP;
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Hydrolase; Serine protease.
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-!- SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                  549 RKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RKLYDY
                                                 1 RKLYDY
                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKLYDY 78
                                                                                                                                                                                                                                                                                     M74220; AAA36451.1;
P00747; 2PK4.
                                                                6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00134; TRYPSIN_HIS; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                           IPR001314; Chymotrypsin. IPR000001; Kringle. IPR003014; PAN.
                                                                                               Serine protease; Signal.

1 19 POTENTIAL.

20 810 PLASMINOGEN.

810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36791 MW;
                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               01,
19,
                                                                                                                                                                                                                                                                                                                PEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6;
Pred. No.
                                                                         Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C7DC06E03B965286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                      plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
                                                                                                                                                                                                                                                                                                               FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
16;
                                                                          DB 4;
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 334;
                                                                                 Length 810
                                                                                                                                                                                                                                                                                                                                                       Lawrence G.M.P.,
                                                                                                                                                                                                                                                                                                               ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                     aglycoplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                  0;
RESULT 4
Q91WJ5
ID Q91W
AC Q91W
DT 01-D
                                                                                                                                                                            В
                                                                                                           Ωy
                Q91WJ5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
 Mus musculus (Mouse)
          PLASMINOGEN.
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Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                  SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis aut receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
Q91WJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9R0W3;
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                    PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ242649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMINOGEN
                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                   Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001400;
InterPro; IPR001254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00747; 1P
MEROPS; S01.233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
                                                                                    549 RKLYDY 554
                                                                                                                     1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                    ; SM00130; KR; 4.
; SM00473; PAN_AP;
; SM00020; Tryp_SI
                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000001;
                                                                                                                                                                                                                   20
812 Å
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1PMK.
                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB46014.1;
                                                                                                                                                                                                                                                                                                                                                                                                        PAN_AP; 1.
                                                                                                                                                                                                                                     19
812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypsin.
le; 5.
                                                                                                                                                                                                                     90535 MW;
                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan_app.
SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kringle
                                                                                                                                                      0;
                                                                                                                                                                  Score 6;
Pred. No.
                                                                                                                                                                                                                     PLASMINOGEN.

8C703C51410EBC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      812
   812
                                                                                                                                                                  DB
34;
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                                                                                                                                                      0;
                                                                                                                                                                                    Length 812;
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                                                                                                                                                      0;
                                                                                                                                                      Gaps
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

19, 19, 19,

Created)
Last sequence up
Last annotation

update)

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RESULT 5
209PA65
ID 09PR
AC 09PR
AC 09PR
AC 09PR
AC 09PR
AC 01-M
DT 01
PRESULT 6
Q9X318
ID Q9X3
AC Q9X3
AC Q9X3
DT 01-M
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                           Q9X3B8;
01-NOV-1999 (
01-NOV-1999 (
01-MAY-2000 )
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC014773; AAH14773.1; -.
SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TremBLrel. 15, 01-OCT-2000 (TremBLrel. 15, 01-MAR-2001 (TremBLrel. 16, HYPOTHETICAL PROTEIN UU080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 407:757-762(2000).
EMBL; AE002107; AAF30485.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 72 AA; 8562 MW; 5DFD611B9A9554B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SEROVAR 3;
MEDLINE-20500219; PubMed-11048724;
Glass J.I., Lefkowitz E.J., Glass J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ureaplasma parvum (Ureaplasma urealyticum biotype
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PR65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PR65
                                                                                                                                                                                                                                                             Plasmid pMD136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urealyticum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasmataceae; Ureaplasma.
                               STRAIN-ATCC43200;
Kantor A., Mett A., Shapira R.;
                                                                                                                                                            NCBI_TaxID=1255;
                                                                                                                                                                                                  Pediococcus
                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of the mucosal
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 RKLYDY 554
Pediococcus pentosaceus pediocin A encoding plasmid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RKLYD 5
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
100.0%;
                                                                                                                                                                                                                                     Bacillus/Clostridium group; Lactobacillaceae,
                                                                                                                                                                                                                                                                                                                                                              12,
13,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 5;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
o. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogen
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EMBL; AF033858; AAF22854.1; -.
Plasmid; Hypothetical protein.
SEQUENCE 73 AA; 8526 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giacomini A., Squartini A., Nuti M.P.; "Nucleotide sequence and analysis of plasmid pMD136 from Pedi- ococcus pentosaceus FBB61 (ATCC43200) involved in Pediocin A production."; Plasmid 0.0-0(2000).
                                                                                                                                                                                                                                                                                      Complete SEQUENCE
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01-DEC-2001 (TrEMBLrel.
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01-OCT-2000 (TREMBLIEL 15, L
01-DEC-2001 (TREMBLIEL 19, L
PUTATIVE PERIPLASMIC PROTEIN.
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Samson D., Roux V., Cossart P., Weissenbach J.,
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Rickettsiaceae; Rickettsieae;
                               Campylobacter.
NCBI_TaxID=197;
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SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                       Bacteria; Proteobacteria;
                                                                Campylobacter jejuni
                                                                            CJ1456C
                                                                                                                                Q9PMK4;
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eae; Rickettsia.
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032180;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
YUSN PROTEIN.
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Perna N.T., Mayhew G.F., Posfai G., Elliott S., Donnenberg M.S.,
Kaper J.B., Blattner F.R.;
"Molecular evolution of a pathogenicity island from enterohemorrhagic Escherichia coli O157:H7.";
Infect. Inmun. 66:3810-3817(1998).
EMBL; AF022236; AAC38366.1; -.
EMBL; AF071034; AAC38366.1; -.
                                                                                                                                             032180
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MEDLINE-98.54123; PubMed-95.93291;
Elliott S.J., Wainwright L.A., McDaniel T.K.,
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 12.3 KDA PROTEIN L0052 (ORF3).
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"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                Q9VAW7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation update)
CG17856 PROTEIN.
                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                 Q9VAW7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; Z99120; CAB15275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.

Bacteria; FirmLoutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%; Score 5; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17FE812FBE408253 CRC64;
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                                    Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases.
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RESULT 12
Q9YXI
ID Q9YXI
AC Q9YXI
AC Q9YXI
AC O1-MA
DT 01-MA
DT 01-JU
DE CG356
GN CG356
OS D1rosc
OC Enkar
OC Ptery
OC Ptery
OC Ephyd
OX NCBI.
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Charly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Sangders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Rainert K., Remington K.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Kathan G.S., Pah S., Jahan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Kathan G.S., Pah S., Jahan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Kathan G.S., Pah S., Shon M., Shugski M.P., Smith H.O.,
RA Zheng X.H., Kathan G.C., Stapheton M., Zhang G., Zhao Q., Zheng L.,
Ra Zheng X.H., Kathan G.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                O9VXI6 PRELIMINARY;
O9VXI5;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                           CG3560.
                                                                                                                                                                                                                                           CG3560 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0039576; CG17856. InterPro; IPR003197; UCR_14kD. Pfam; PF02271; UCR_14kD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%; Score 5; 1
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          839BE06F2E1B05D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferriac C., Ferriac S., Fleischmann W.,
RA Glodek A., Goup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Barris N.L., Harvey D., Heiman T.J., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kniston D.L.,
RA Mchulov G., Wilshna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Wilshna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Shue B.C., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinnstock G.M., Weissenbach J.,
RA Shue B.C., Woodage T., Worley K.C., Wu D., Ya
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                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Ewissen S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ESTROGEN RECEPTOR RELATED PROTEIN 3 (FRAGMENT).
                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 1:
TISSUE-BRAIN;
                   SEQUENCE FROM N.A
                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                          Q9UNJ4;
                                                                                                                                                                                                                                                                              Q9UNJ4
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                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR003197;
                                                                                                                                                                                                                                                                                                                                                                                         52 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                          1 RKLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF02271; UCR_14kD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserve
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111 AA; 1
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13568 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UCR_14kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.3%; Score 5; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                    Catarrhini;
                                                                                                        Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                              129
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o. 87;
                                                                                                                                                                                                                                                                            AA
                                                                                    Hominidae;
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Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLR3958.
Rhizobium loti (Mesorhizobium loti).
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000182; Acetyltransf_GCN5.
Iffam; PF00583; Acetyltransf; 1.
Transferase; Complete proteome.
SEQUENCE 148 AA; 17075 MW; A59FAEB2
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MEDLINE-21082930; PubMed=11214968;
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HSSP; P11746; IMNM.

HSSP; P11746; IMNM.

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InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21; Search time 4.66667 Seconds (without alignments) 49.782 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-657-431-11 34 1 RKLYDY 6

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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MEDLINE=97238710;
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PubMed=9102221;
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Rickli E.E.;
                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 183-354
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                                                                         "Solution structure of the kringle 4 domain 11 nuclear magnetic resonance spectroscopy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure and ligand binding determinants of the recombinant kringle 5 domain of human plasminogen.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461
                                                                                                                                                                                                                                                                                        25]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y., Mochalkin I., McCance
                                                                                                                                                                                                                                                                                                      Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
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 Α.,
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Espling E.S.,
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                                                            212:541-552(1990).
                               AND THR-620
                                                                                                                                                                                                                                                                                                     221:939-949(1994).
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              PubMed=1986355;
                                                                                                                                                                                                                                                       PubMed=8652577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9521645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1657149;
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 J.,
                                                                         domain from human poscopy and distance
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 Saito H.,
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 RESULT 2
PLMN_MOUSE
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                                                          use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.institutions.com/or send an email to licensease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17,
01-FEB-1991 (Rel. 17,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P20918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pogen S.J., Bell S.M., Schaefer L.A., Elliott R.W.; "Characterization of the cDNA coding for mouse plasminogen localization of the gene to mouse chromosome 17."; Genomics 8:49-61(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasminogen
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EMBL; J04766; AAA50168.1;
PIR; A38514; A38514.
HSSP; P00747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION OF ANGIOSTATIN, MEDLINE=95042728; PubMed=7525077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91184812; PubMed=2081600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549
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                                                                                                                                                                                                                    ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANDOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANDOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION MISCELLANDOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE BURDELY ACTIVATED BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
                                                                                                                                                                                                                                                                                                                                                                                                 METASTATIC TUMORS IN VIVO.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATOR, COLLAGENASES AND SEVERA AS C1 AND C5. IT CLEAVES FIBRIN, I LAMININ AND VON WILLEBRAND FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS
                                                                                                                                                                                                           TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKLYDY 6
                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Rodentia;
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Pred. No.
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Sciurognathi; Muridae;
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16;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
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Matches
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SMART; SM00473; PAN_AP; 1.
SMART; SM00020; TIYP_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00051; kringle; 5.
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MGD; MGI:97620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00089; trypsin; 1.
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InterPro; IPR001254;
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Similarity 6; Conserv
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                                                                                                          582
103
184
275
377
Conservative
                                 AA;
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90846 MW;
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       100.0%;
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                                        INTERCHAIN (BY SIMILARITY).
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CHARGE RELAY SY
BY SIMILARITY
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KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
0;
       Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                              PLASMIN SHORT FORM OF CHAIN ANGIOSTATIN.
                                                                                                                                                                                                                                                              CHARGE
                                                                                                                                                                                                                                                                      SERINE
                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE
                                 D34A74A4FC2256F8 CRC64;
 Mismatches
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E RELAY SYSTEM
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                1;
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Zymogen; Signal.
                Length 812;
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GFO_ZYMMO
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YFL1_YEAST
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Best Local
                                                                                                                                                                                 Matches
Q07982;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                  GFO_ZYMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96287652; PubMed-8686379;
Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I.,
Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
"Analysis of a 36.2 kb DNA sequence including the right telomere chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyan Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                     Hypothetical protein; Chaperone; Signal. SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor.
YFR041C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 34.2 kDa protein in SAP155-YMR31 intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P43613;
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 12:149-167(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 10:261-268(1995).
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P25685;
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                                                                                                                                                                                                                                          295 AA;
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                         42
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                                                                                                                                                                                                                                                                                                                                                                                                                  BAA09280.1;
BAA08007.1;
                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                       20
295
110
                                                                                                                                                                                             94.1%;
83.3%;
                                                                                                                                                                                                                                          34191 MW;
 Last sequence update)
                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                           Score 32;
                                                                                                                                                                                                                                                       J-DOMAIN
                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN YFR041C
                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                        4541BF6C353DB8AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                               439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 AA.
                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                0;
                                                                                                                                                                                                           Length 295;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yokoyama K.,
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RESULT 5
RL5_METJA
AC ID
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                                                                                                                                                                                                                                                                                                 Matches
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P54040;
                        RL5_METJA
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M97379; AAA27690.1; -. EMBL; X73088; CAA51534.1; -. PDB; 10FG; 21-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suiss Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucitol.
-:- COFACTOR: CONTAINS ONE TIGHTLY-BOUND NADP(H) MOLECULE PER SUBUNIT.
-:- PATHWAY: SORBITOL-GLUCONATE PATHWAY.
-:- SUBUNIT: HOMOTETRAMER.
-:- SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mobilis: an osmoprotective periplasmic enzyme containing dissociable NADP.";
Structure 4:1413-1428(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01408; GFO_IDH_MocA; 1.
Pfam; PF02894; GFO_IDH_MocA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000683; GFO_IDH_MocA_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loos H., Sahm H., Sprenger G.A.;
"Glucose-fructose oxidoreductase, a periplasmic mobilis, is active in its precursor form.";
FEMS Microbiol. Lett. 107:293-298(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-71 FROM N.A., AND SEQUENCE OF 2-16 AND 53-71 STRAIN=ATCC 29191 / ZM6, AND ATCC 31821 / ZM4 / CP4; MEDLINE=93231476; PubMed=8472911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanagasundaram V., Scopes R.K.; "Cloning, sequence analysis, and expression of the structural gene encoding glucose-fructose oxidoreductase from Zymomonas mobilis."; J. Bacteriol. 174:1439-1447(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The structure of glucose-fructose oxidoreductase from Zymomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97148336; PubMed-8994968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zymomonas.
NCBI_TaxID=542;
                                                                                                                                                                               133 RKIYDY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: D-glucose + D-fructose = D-gluconolactone + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymomonas mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucose--fructose oxidoreductase precursor (EC 1.1.99.28) (GFOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                       Local Similarity tes 5; Conserv
                                                                                                                                                                                                                                      1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                               53
61
439 AA;
                                                                                                                                                                                                                                                                                                 Conservative
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              439
61
                                                                                                                                                                                                                                                                                                                                                                                                               47801 MW;
                                                                                                                                                                                                                                                                                                                         94.18;
83.38;
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    Mismatches

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L -> Q (IN REF. 2; AA SEQUENCE).
; C1E4A19F5B34267A CRC64;
                                                                                                                                                                                                                                                                                                                         Pred. No.
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                           190 AA
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                     Length 439;
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01-OCT-1996
16-OCT-2001
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MEDLINE-96337999; pubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougharty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S. M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                       Q9XDS7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequing 16-OCT-2001 (Rel. 40, Last annotation to the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00281; Ribosomal_L5; 1. Pfam; PF00673; Ribosomal_L5_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jannaschii.";
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPL5P OR MJ0469.
Methanocom
"Streptococcus intermedius enolase gene."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                               Sato
                                                                                        SEQUENCE FROM N.A. STRAIN-ATCC 27335;
                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1338;
                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                            Streptococcus intermedius
                                                                                                                                                                                                                                                                                                                glycerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENO_STRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein;
SEQUENCE 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001076; Ribosomal_L5; 1.
PROSITE; PS00358; RIBOSOMAL_L5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MJ0469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67497; AAB98458.1; -.
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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34,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%;
83.3%;
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Last annotation update)
(2-phosphoglycerate dehydratase)
                                                                                                                                                                                                                               Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation L5P.
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                                                                                                                                                                                                                          Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                       (2-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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PROSITE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium
ACT_SITE 155 155
METAL 242 242
METAL 291 291 MJ
METAL 318 318 MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (
16-OCT-2001 (
Enolase (EC (
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-SF370 / ATCC 700294 / Serotype M1;

MEDLINE-21192684; PubMed-11296296;

MEDLINE-21192684; PubMed-11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycerate hydro-lyase).
ENO OR SPY0731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P82479;
16-OCT-2001
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-i- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZIN
                                        Submitted (MAY-2000) to
                                                                                                                                                                          STRAIN=JRS4 / Serotype M6;
Hogan D.A., Du P., Stevenson
                                                                                                                                                                                                                                                    PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
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-!- PATHWAY: GLYCOLYSIS.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                VanBogelen R.A.
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                                                                                                       'Two-dimensional gel electrophoresis map of
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nitted (MAY-2000) to the SWISS-PROT data bank.
CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00113;
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                                                                                                                                                                                                                                                    SEQUENCE, AND MASS SPECTROMETRY
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(Rel. 40, Last annotation update)
4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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There are no restrictions on
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                                                                                                                                                                              G.W.,
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RESULT 8
Y140_M
ID Y140_M
AC P75033
DT 01-NOV
DT 16-OCT
DE HYDOTH
GN MYCOPL
OC MYCOPL
OX MCBI_T
RN [1]
RP SEQUEN
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01-NOV-1997
16-OCT-2001
                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EWBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and institutions as the statement is not removed.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical ATP-binding protein MG140 homolog MPN153 or MP001.
   EMBL; AE000001; AAB95649.1; -.
                                                                                                                                                                                                                                               Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P75033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00148; ENOLASE.
ProDom; PD000902; Enolase;
PROSITE; PS00164; ENOLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: GLYCOLYSIS.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic (By simi.
-i- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                  Nucleic Acids Res.
                                                                                                                                                                                                 pneumoniae."
                                                                                                                                                                                                                 "Complete sequence analysis of the genome
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase;
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COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
                                                                                                                                                              SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P00924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycolysis; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss Institute of Bioinformatics and the EMBL outstatute Swiss Institute. There are no restrictions on the EMBL outstatute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AA;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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    Mismatches

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MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1113 AA
                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                 of the bacterium
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Best Local
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                            P34881;
01-FEB-1994
                                                                                                                                                                                                                                                                                        Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                  Zinc-finger.
ZN_FING 1
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. V1rol. 74:3815-3831(2000).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Afonso C.L., Tulman E.R., Lu Z., "The genome of fowlpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; ATP-binding; Helicase; Complete proteome NP_BIND 313 320 ATP (POTENTIAL).
                                                           DNM1_ARATH
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     EMBL; AF198100; AAF44533.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20193820; PubMed=10729156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowlpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP0132 OR FPV189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9J544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001
16-0CT-2001
                                                                                                                                  647 KKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 RRLYDY 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 5; Conserv
                                                                                                                                                             1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOWPV
                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1113 AA;
                                                                                                                                                                                                                                                  1161 AA;
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 (Rel.
(Rel.
(Rel.
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                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIS ENZYME CONSISTS OF AT LEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FPV)
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
. 28, Created)
. 28, Last sequ
. 41, Last anno
                                                                                                                                                                                                                                               1098 C4:
A; 133468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
83.3%;
                                                                                                                                                                                                        91.2%;
83.3%;
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                                                                                                                                                                                                                       Score 31;
                                                                                                                                                                                                        Pred. No. 93;
                                                                                                                                                                                                                                                                C4-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1161 AA
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                  334C2FC5DD63584F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48A3337EB0E81A40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zsak L., Kutish G.F.,
                                                           1534 AA
                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                      1; Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIGHT SUBUNITS
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01-FEB-1994 01-MAR-2002

Last annotation update) Last sequence update)

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RESULT 11
G10_XENLA
ID G10_X
AC P1286
DT 01-OC
DT 01-JU
DE G10 F
OS Xenop
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                                01-OCT-1989
01-OCT-1989
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seve physically assigned Pl and TAC clones."; DNA Res. 5.379-391(1998).
-I- FUNCTION: METHYLATES CG RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. COLUMBIA;
MEDLINE=99156233; PubMed=10048488;
Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finnegan E.J., Dennis E.S.;
"Isolation and identification by sequence homology of a putative cytosine methyltransferase from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
MEDLINE=93281384; PubMed=8389441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATHIM OR AT5G49160 OR K21P3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methyltransferase AthI) (DNA Metase AthI) (M.AthI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (cytosine-5)-methyltransferase AthI (EC 2.1.1.37) (DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF001426; BAH; 2.
Pfam; PF00145; DNA_methylase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 21:2383-2388(1993).
                                                                                                G10_XENLA
                                                                                                                                                                                                                                                                                                                                  Transferase; Methyltransferase; ACT_SITE 1198 1198 BY
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00094; C5_MTASE_1; 1. PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00439; BAH;
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0105; C5METTRFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REBASE; 2839; M.AthI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L10692; AAA32829.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
Xenopus laevis (African clawed frog)
                 G10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rabata S.;
                                                                                                                                                                                   172 RKVYDY 177
                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
homocysteine + DNA containing 5-methylcycosine.
SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
SIMILARITY: CONTAINS 2 BAH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB016872; BAB10334.1; -.
                                                                                                                                                                                                                                                 Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001025; BAH.
IPR001525; C5_DNA_meth.
                                                                                                                                                                                                                                                                                                                 1198 1:
1534 AA;
                             (Rel. 12, Created)
(Rel. 12, Last seq
(Rel. 29, Last ann
                                                                                                                                                                                                                                                 Conservative
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                    83.3%;
                                                                                                                                                                                                                                                                                                                    172430 MW;
                                Last sequence up
                                                                                                                                                                                                                                                               Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                 DNA-binding.
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                  23FC944AA7074C5A CRC64;
                                                  update)
                                                                                                    144 AA
                                                                                                                                                                                                                                                                    1.2e+02;
                                                                                                                                                                                                                                                                                  DB 1;
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           PLMN_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McGrew L.L., Dworkin-Rastl E., Dworkin M.B., Richter J.D.; "Poly(A) elongation during Xenopus oocyte maturation is requitranslational recruitment and is mediated by a short sequence
MEDLINE-90175323; PubMed-2626424;

Schaller J., Straub C., Kaempfor U., Rickli E.E.;

"Complete amino acid sequence of canine miniplasminogen.";

Protein Seq. Data Anal. 2:445-450(1989).

-i. PUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS
A PROTECLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
EMBRYONIC DEVELOPMENT, TISSUE REMODELING, THOR INVASION,
AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Nuclear (Potential).

-i- DEVELOPMENTAL STAGE: OOCYTE MATURATION IS ACCOMPANIED
-RECRUITMENT OF SPECIFIC MATERNAL MRNAS INTO POLYSOMES.

EXAMPLE OF A PROTEIN WHICH IS TRANSLATED AT THAT TIME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes Dev.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD009460; G10; 1.
PROSITE; PS00997; G10_1; 1.
PROSITE; PS00998; G10_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01125; G10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X15243; CAA33321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLMN_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001748; G10.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P80009;
                                                                                                                                                                                                                                                             fissue=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 RELYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S05955;
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(Rel.
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(EC 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20, Created)
20, Last sequence update)
40, Last annotation update)
.4.21.7) (Fragment).
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119
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                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein; Zinc-finger.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCOMPANIED E
TO POLYSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑN
                                                                                                                                AS
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RESULT 13
PLMN_SHEEP
                                                                                                                                                                                        В
                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                        15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051; kringle; 1.

Pfam; PF00089; trypsin; 1.

SMART; SM00130; KR; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 1.

PROSITE; PS50240; TRYPSIN_DOW; 1.

PROSITE; PS00134; TRYPSIN_HS; 1.

PROSITE; PS00135; TRYPSIN_HS; 1.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                               P81286;
15-DEC-1998
  Bovidae;
                                     Ovis aries (Sheep).
                                                                                                                           PLMN_SHEEP
                                                                                                                                                                                                                                                                                                                                       SITE
                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000001;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.
                                                                                                                                                                                        72 RKLFDY 77
                                                                                                                                                                                                               1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREPTOKINASE.

STREPTOKINASE.

MISCELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN

IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

TRYPSIN FAMILY. PLASMINGEN SUBPAMILY.

STMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ AND VON WILLEBRAND FACTOR.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUN FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATOR, CO. AS C1 AND C5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      remodeling;
                                                                                                                                                                                                                                      5
Caprinae; Ovis
                                                                                                                                                                                                                                                  Similarity
                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
(EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                     333 AA;
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                      25
54
90
100
130
222
252
252
279
145
188
188
188
188
188
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood
                                                                                                                                                                                                                                                                                     36678
                                                                                                                                                                                                                                                 88.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation; Kringle; Zymogen.
                                                                                                                                                                                                                                                                                      Œ,
                                                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).
                                                                                                                                                                                                                                  Score 30; DB
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                 (BY
                                                                                                                                                                                                                                                                                                           SITE OF SUBSTRATE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMIN HEAVY CHAIN PLASMIN LIGHT CHAIN KRINGLE 5.
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                    C8C0271B6C6AC8D4 CRC64;
                                                                                                                                                                                                                                                                                               SIMILARITY )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEASE.
                                                                                                                        343 AA
                                                                                                                                                                                                                                                           DB 1; Length 333;
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽.₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOUND TO
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QF
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 0;
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ROCCOS GREET DE LAC
                                                                                                                                                             YK96_AERPE
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                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00051; kringle; 1.

Pfam; PF00089; trypsin; 1.

SMART; SM00103; KR; 1.

SMART; SM001020; Tryp_SPC; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
          NCBI_TaxID=56636;
                                   Aeropyrum pernix.
Archaea; Crenarchaeota;
                                                                                          30-MAY-2000
16-OCT-2001
                                                                                                                    Q9YA42;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                        Aeropyrum.
                                                                  APE2096
                                                                             Hypothetical
                                                                                                                                                 YK96_AERPE
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAMININ AND VON WILLEBRAND FACTOR.

- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000001;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schaller J., Straub C., Kampfer U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93149995; PubMed=1492092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete amino acid sequence of ovine miniplasminogen.";
                                                                                                                                                                                                                    83 RKLFDY 88
                                                                                                                                                                                                                                  1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEIN SEG. Data Anal. 5:21-25(1992).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS APPORTED. THE FUNCTION IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRADELAND FOLLICLE. IT ACTIVATES THE WALLS OF THE GRADELAND FOLLICLE. IT ACTIVATES THE UNKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              remodeling; Blood
                                                                                                                                                                                                                                                                        Similarity 83.5; Conservative
                                                                                                                                                                                                                                                                                                                              343
                                                                            (Rel. 39, Created)
(Rel. 39, Last sequence
(Rel. 40, Last annotatic)
l protein APE2096.
                                                                                                                                                                                                                                                                                                                                           343
                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                        140
>343
17
120
341
181
181
224
319
                                                                                                                                                                                                                                                                                   88.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                              37662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kringle
                                  Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coagulation; Kringle;
                                                                                                                                                                                                                                                                                                                              WW.
                                                                                         annotation update
                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                     Score 30; DB
Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            KRINGLE 4. KRINGLE 5.
                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGHT CHAIN A.
                                                                                                                                                                                                                                                                                                                           8DF6EBA92D596EE0 CRC64;
                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickli E.E.;
                                                                                                                                               426 AA
                                                                                                                                                                                                                                                                                   DB 1; Length 343;
                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymogen
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                     0;
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RESULT 15
SIK1_YEAST
ID SIK1_YEAST
ID SIK1_YE
OC 012460
DT 01-NOV
DT 16-OCT
DE SIK1 P
GN SICHA
OC SUKARY
OC SACCHA
OX NCBI_T
RN [1]
RP SEQUEN
RC STRAIN
RA MOTION
RA MOTION
RA MOTION
RA MOTION
RA FEVELL
RA FEVELL
RA JOHNST
RA JOHNST
RA WOHIGH
RA W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 5
                                                                                                              SEQUENCE PAND .....

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Mardis E., Menezes S., Johnston L., Nan M., Pauley A., Peluso D., Rifken L., Riles L., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence updi
16-OCT-2001 (Rel. 40, Last annotation updi
SIK1 protein (Nucleolar protein NOP56).
SIK1 OR NOP56 OR YLR197W OR L8167.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002936; Toprim.
Pfam; PF01751; Toprim; 1.
SMART; SM00493; TOPRIM; 1.
   CHARACTERIZATION, MEDLINE=98038777;
                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morin P.J., Downs J.A., Snodgrass A.M., "Genetic analysis of growth inhibition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96040178; PubMed=7547500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q12460;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIK1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crenarchaeon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ku Hosoyama A., Fukui S., Nagai Y., Nishijina K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000063; BAA81107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE UPF0095 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    Growth Differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELYDY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aeon, Aeropyrum pernix K1.";
6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                     (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al protein; Complete proteome.
426 AA; 47681 MW; 73A0B78FCD1206B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
      PubMed=9372940;
                           AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                    6:789-798(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilmore T.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAL4-L kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haikawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kosugi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Search completed: November Job time: 6.66667 secs

8

09:33:54

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                                                                  Query Match
Best Local 9
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gautier T., Berges T., Tollervey D., Hurt E.;
"Nucleolar KKE/D repeat proteins Nop56p and Nop58p interact with Nop1p and are required for ribosome biogenesis.";
Mol. Cell. Biol. 17:7088-7098(1997).
-i- FUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT SYNTHESIS.
                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                      Pfam; PF01798; Nop; 1. ProDom; PD004104; Nop; 1.
                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                   entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: INTERACTS WITH NOP1 AND NOP58.
-i- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-i- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
                                                                                                                                           MUTAGEN
                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                  SGD; S0004187; SIK1.
InterPro; IPR002687; Nop.
                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                             Ribosome biogenesis;
286 RQLYDY
                            1 RKLYDY
                                                                                                                                                                                                                                                                                                                U20237; AAC49066.1;
U14913; AAB67431.1;
                                                      Similarity 5; Conserv
                                                                                                               504
 291
                            6
                                                                                                                                                                                                                  3
3
3
                                                        Conservative
                                                                                                                                           385
                                                                                                                                                                                      355
                                                                                                               AA;
                                                                                                                                         385
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                                                                                                                                                                                                               504
333
                                                                  88.2%;
83.3%;
                                                                                                               56864
                                                                                                                                                                                                                                             Nuclear
                                                                                                                MW.
                                                        ۲,
                                                                    Score 30;
Pred. No.
                                                                                                             M->R: REDUCED GROWTH RATE AT ALL TEMPERATURES; WHEN ASSOCIATED WI; F8522A5870EF4842 CRC64;
                                                                                                                                                                                   ASP/GLU/LYS-RICH.

Y->A: REDUCED GROWTH RATE AT ALL
TEMPERATURES; WHEN ASSOCIATED WITH R-385
Y->C: AT 37 DEGREES, GROWTH SLOWS AFTER (
                                                                                                                                                                                                                                             protein.
                                                                                                                                                       TO 8 HOURS AND CELL DIVISION STOPS 20 HOURS.
                                                        Mismatches
                                                               DB
66;
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                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                        0,
                                                                                   Length 504
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                     by and for
                                                                                                                              WITH A-333
                                                        0
                                                      Gaps
                                                                                                                                                                      AFTER
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                                                      0;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:22; Search time 14.3333 Seconds (without alignments) 72.416 Million cell updates/sec

Title: Perfect score: Sequence: US-09-657-431-11 34 1 RKLYDY 6

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungl:*
4: sp_human:*
5: sp_human:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel.
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_virus:*
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_bacteri
17: sp_archeap sp_archea:*
sp_bacteria:*
sp_fungi:* sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rolant:*
sp_rolant:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	ر ت	4	ω	2	1	Result
31	31	31	31	31	31	31	31	32	32	32	32	34	34	34	34	Score
91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	94.1	94.1	94.1	94.1	100.0	100.0	100.0	100.0	Query Match
454	434	434	417	417	409	388	274	433	404	254	73	812	812	810	334	Query Match Length
10	16	N	16	N	16	9	ഗ	N	16	16	12	11	11	4	6	ВВ
Q9ZRW0	Q97QS2	Q935W7	050899	Q45037	Q99TG1	Q38198	P91014	P75002	Q9KVG1	Q9PMJ3	Q07273	Q91WJ5	Q9R0W3	Q15146	046507	ID
Q9zrw0 cicer ariet	Q97qs2 streptococc	Q935w7 streptococc	O50899 borrelia bu	Q45037 borrelia bu	Q99tg1 staphylococ	Q38198 xanthomonas	P91014 caenorhabdi	P75002 zymomonas m		Q9pmj3 campylobact	Q07273 turkey rhin	Q91wj5 mus musculu	Q9r0w3 rattus norv	Q15146 homo sapien	O46507 papio hamad	Description

45	44	43	42	41	40	39		37			34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
29	29	29	29	29	29	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	31	31	31	31	31	31	31	31
ū	85.3	.5	5	85.3				88.2																				91.2
170	157	148	146	104	73	1436	1187	732	722	647	502	474	405	405	320	319	294	292	160	144	1519	1517	1404	1165	633	584	522	499
N	10	16	11	16	12	w	10	2	S	ψ	16	17	16	9	ഗ	16	16	16	17	σı	10	10	10	12	տ	տ	10	10
Q9KX31	Q9AUJ1	Q98F36	Q924Q3	Q9PMK4	Q90089	Q07527	Q9ZV43	Q9L281	Q9V5F2	044560	Q9PQW1	028424	031948	064073	Q18887	Q97DR3	Q99ZF5	Q97QJ3	Q97CJ1	097454	023273	Q9SEG3	Q9T011	Q98839	097305	8M0060	Q9SGT7	Q9LTV0
Q9kx31 streptococc	Q9auj1 oryza sativ			Q9pmk4 campylobact	Q90089 turkey rhin	Q07527 saccharomyc	Q9zv43 arabidopsis		Q9v5f2 drosophila		Q9pqw1 ureaplasma	028424 archaeoglob	031948 bacillus su	064073 bacteriopha	റ		Q99zf5 streptococc	Q97qj3 streptococc	Q97cj1 thermoplasm	097454 drosophila			Q9t0il arabidopsis	Q98839 molluscum	097305 plasmodium		Q9sgt7 arabidopsis	Q9ltv0 arabidopsis

ALIGNMENTS

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RESULT 3
Q9ROW3
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Q15146
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Best Local Similarity
"here 6; Conserva
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                                                                                 Matches
                                                                                          Query Match
Best Local
                                                                                                                                        SMART; SM00130; KR; 5.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; TryP_SPc; 1.

SMOSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50040; TRYPSIN_BOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Signal; SIGNAL 1 19
                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
PLASMINOGEN PRECURSOR.
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                EMBL; M74220; AAA36451.1; HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                                                                                                                                     Browne M.J., Chapman C.G., Dodd I., Carey Mitchell D., Robinson J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                              InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                         Fibrinolysis 0:0-0(1991)
                                                                                                                                                                                                                                                                                                                                                                                                    HeLa cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q15146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q15146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                         549
                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                           "Expression of recombinant human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 RKLYDY 78
                                                           1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                     TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE
                                         RKLYDY 554
                                                                                                                                                                                                                                                                 PF00024; PAN; 1. PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                   PF00051; kringle; 5.
                                                                            9,
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                  IPR001314; Chymotrypsin. IPR000001; Kringle. IPR003014; PAN.
                                                                                                                       20
810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 AA;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                       810 I
90555 MW;
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01,
19,
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                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                               Score 34; DB
Pred. No. 61;
0; Mismatches
                                                                                                                                 POTENTIAL.
PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C7DC06E03B965286 CRC64;
                                                                                                                       B05C7D4B0D020B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                              FAMILY S1;
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                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ
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on update)
                                                                                                                                                                                                                                                                                                                                                                                                                              J.E.,
                                                                                                   4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                 Length 810;
                                                                                                                                                                                                                                                                                                                                                                               ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence G.M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                          aglycoplasminogen
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RESULT 4
Q91WJ5
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Best Local :
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SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS500134; TRYPSIN_HLS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001400; SOMATOTROP.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00118; KRINGLE.
                       Q91WJ5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ROW3;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                        CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
EMBL; AJ242649; CAB46014.1; -.
HSSP; P00747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91250378; PubMed-1645711;
Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis autoantigen (GP330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=LIVER;
Bangert K., Johnsen A.H., Thorsen S.;
Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
Mus muscu⊥us (Mouse).
             PLASMINOGEN
                                                                          Q91WJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLASMINOGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS;
                                                                                                                                        549 RKLYDY
                                                                                                                                                                1 RKLYDY
                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S01.233
                                                                                                                                                                                                     Similarity
                      (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                        20
812 ‡
                                                                                                                                                                                                                                                                 Serine protease;
                                                                                                                                        554
                                                                                                                                                                6
                                                                                                                                                                                         Conservative
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                        812
90535 MW;
                                                                                                                                                                                                    100.0%;
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SOMATOTROPIN
                        19,
19,
                                                                                                                                                                                                                                                                             Signal.
                      Last sequence update)
Last annotation update)
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                                                 Created)
                                                                                                                                                                                                                                        PLASMINOGEN.
; 8C703C51410EBC9E CRC64;
                                                                                                                                                                                                    Score 34;
Pred. No.
                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                         Indels
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RESULT
Q07273
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Best Local S
Matches 6
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Q07273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014773; AAH14773.1; -.
SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-EB-1997 (TrEMBLrel. 02, Last annotation updat
HYPOTHETICAL 8.5 KDA PROTEIN IN 22K 3 REGION.
Turkey rhinotracheitis virus (TRTV).
         SEQUENCE FROM N.A.

STRAIN-NCTC 11168;

MEDLINE-20150912; PubMed=10688204;

MEDLINE-20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S

Basham D., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;
                                                                                                                                                                                               Q9PMJ3;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
HYPOTHETICAL PROTEIN CJ1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu Q., Davis P.J., Brown T.D.K., J. Gen. Virol. 73:1355-1363(1993) EMBL; X63408; CAA45005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Metapneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 73 AA; 8488 MW;
                                                                                                                                                                                                                                                                  О9РМJ3
                                                                                                                               NCBI_TaxID=197;
                                                                                                                                             Campylobacter
                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                       Campylobacter jejuni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=UK/3BV/85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11264;
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 genome sequence of the food-borne pathogen Campylobacter jejuni
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Similarity 100.0%;
6; Conservative 0
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                                                                                                                                                                                                                                                                   PRELIMINARY;
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83.3%;
                                                                                                                                                            epsilon
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Pred. No.
                                                                                                                                                                                                                                         Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           D6E09B8BDC40EC4F CRC64;
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                                                                                                                                                            subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                   254 AA.
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                                      Holroyd S., C.W.,
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Nature 403:665-668(2000).
EMBL; AL139078; CAB73890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

WEDLINE-20406833; PubMed=10952301;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.

Ermolaeva M.D., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KVG1;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete SEQUENCE 254 AA; 30201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPOSASE,
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                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR.
                                                                                                                                                                                                                                                      P75002;
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VC0185.
Wiegert T., Sahm H., "The substitution of
                                                                                                                                                                                                             GFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).
EMBL; AE004108; AAF93361.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
                                               STRAIN-ZM6;
                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                   Zymomonas mobilis
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                                                                       SEQUENCE FROM
                                                                                                                  NCBI_TaxID=542;
                                                                                                                                             Zymomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 RKIYDY 215
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83.3%;
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Pred. No.
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    G.A.; amino
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15712EC3A70AD3E1 CRC64;
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         acid residue
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48;
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         alters
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""atrhes 5; Conserv:
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                                                                                             Matches
                                                                                                                   Query Match
Best Local
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STRAIN-BRISTOL N2;
Du Z., Gattung S.;
"The sequence of C. elegans cosmid C01G8.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80439; AAB3641.2; -.
HSSP; P25685; 1HDJ.
                                                                                                                                                                                 Hypothetical protein. SEQUENCE 274 AA; 32579 MW;
                                                                                                                                                                                                                             PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                      PRINTS; PR00625; DNAJPROTEIN SMART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                  InterPro; IPR003095; DnaJ.
InterPro; IPR001623; DnaJ_N.
Pfam; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 32.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000683; GFO_IDH_MocA. InterPro; IPR004104; GFO_IDH_MocA_C. Pfam; PF01408; GFO_IDH_MocA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing glucose-fructose oxidoreductase of Zymomonas mobilis submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P91014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 RKIYDY 139
85
                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                              1 RKLYDY 6
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RRLYDY
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PF02894;
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                                                                                        5
                                                                                                                 Similarity
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AA;
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
433
47189 MW;
                                                                                                            91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.1%;
                                                                                                            Score 31;
Pred. No.
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Pred. No.
                                                                                                                                                                              8A6F3C7692A572E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13CFADE84794E736 CRC64;
                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA
                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                      0;
                                                                                                                                  Length 274;
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                                                                                   0;
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                                                                                   Gaps
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 Best Local Similarity
Matches 5; Conserv
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                  Pfam; PF00390; malic; 2.
PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; UNKNOWN_1.
                                                                                                                              Lancet 357:1225-1240(2001).
EMBL; AP003134; BAB42791.1; -
EMBL; AP003363; BAB57864.1; -
InterPro; IPR001891; Malic_enzyme
InterPro; IPR00205; NAD_binding.
                                                                                                                                                                                                                    SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SA1524 PROTEIN (MALATE DEHYDROGENASE HOMOLOG).
SA1524 OR SAV1702.
                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus (strain Mu50).
Bacteria; Firmicutes; Bacillus/Clostridium
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                           Complete proteome
                                                                                                                                                                                                                aureus.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus/Staphylococcus group; Staphylococcus NCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99TG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91252299; PubMed=1840658;
Kuo T.T., Tan M.S., Su M.T., Yang M.K.;
"Nucleotide sequence of filamentous phage Cflc from Xanthomonas campestris pv. citri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 19:2498-2498(1991).
EMBL; M57538; AAA32201.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssDNA viruses; Inoviridae; Inovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q38198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 KKLYDY 160
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                                                              409 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 AA;
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                                                              44251 MW;
              91.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42785 MW;
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83.3%;
               Score 31; DB 16;
Pred. No. 1.3e+02;
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Pred. No. 1.2e-
1; Mismatches
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Last annotation update)
                                                             1D88682BD01F1EBD CRC64;
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   Mismatches
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                             Length 409;
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   Indels
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Gaps
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STRAIN-N40;
MEDLINE-95369900; PubMed-7642278;
Feng S., Das S., Lam T., Flavell R.A., Fikrig E.
PA 55-kilodalton antigen encoded by a gene on a
PA 55-kilodalton antigen encoded by a ntibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q45037
Q45037;
                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayt Lathigra R., White O., Ketchum K.A., Dodson R., Hickey Louding R.D., Richardson Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson Doughertson I. Kerlaydson B. Oliver B., Richardson B., Charles B., Richardson B., Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TremBLrel.
01-DEC-2001 (TremBLrel.
S1 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                    Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid 1p54
Bacteria; Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLIEL. 06, 01-JUN-1998 (TREMBLIEL. 06, 01-NOV-1998 (TREMBLIEL. 08,
                                      TIGR;
                                                            Nature 390:580-586(1997).
EMBL; AE000790; AAC66229.1;
                                                                                                                  "Genomic sequence of a Lyme burgdorferi.";
                                                                                                                                                                                    Garland S., Fujii C
Smith H.O., Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi (Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BBA05
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Twmnn. 63:3459-3466(1995).
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                                          Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougharty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=TYPE 2 ATCC 11733;
Bergmann S., Rohde M., Chhatwal G.S., Hammerschmidt S.;
"alpha-enolase of Streptococcus pneumoniae is a plasminogen-binding protein displayed on the bacterial cell surface.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ303085; CAC683091.1; -
CHAIN 2 434 ALPHA-ENOLASE.
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MEDLINE=21357209; PubMed=11463916;
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Bacteria; Firmicutes; Bac
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            Science 293:498-506(2001)
                      pneumoniae.
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                         "Complete genome sequence of a virulent
oneumoniae.":
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DR ITIGR; SP1128; DR128:.

DR PFRM; P900131 emolase: 1.

DR PRISTIE: P800146; EMOLASE: 1.

EMOUNTED 434 AA; 47103 MM; OD64P804BB99C4 CRC64;

SO SROURNE 434 AA; 47103 MM; OD64P804BB99C4 CRC64;

Date Local Similarity 81.3%; Proceed 1: D8 16; Length 434;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 1 RKLTDY 6

Db 253 RW170 258

Search completed: November 8, 2002, 09:36:12

Job time: 16:3333 secs
```



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November ζ. 2002, 09:33:36; Search time 9 Seconds (without alignments) 64.060 Million cell updates/sec

Perfect score: US-09-657-431-11

RKLYDY 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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hypothetical prote	probable flagellar	hypothetical prote	probable periplasm	hypothetical 8.5K	apoprotein(a) (EC	probable membrane	hypothetical prote	6-phosphofructokin	plasmin (EC 3.4.21	plasmin (EC 3.4.21	hypothetical prote	hypothetical prote	phosphoglycerate m	4-hydroxybutyrate	plasmin (EC 3.4.21

ALIGNMENTS

III
smin (EC 3.4.21.7) precursor [validated] - human
dternate names: plasminogen precursor [misnomer]
Ontains: angiostatin; microplasmin; plasminogen
pecies: Homo sapiens (man)
Nate: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
.ccession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627;
etersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
Biol. Chem. 265, 6104-6111, 1990
itle: Characterization of the gene for human plasminogen, a key proenzyme
eference number: A35229; MUID:90202879
ccession: A35229

A04625;

A; Re A; Ac N; Al N; Co C; Sp C; Da C; Ac C; Ac R; Pe A; Ti in the f

A; Molecule type: DNA A; Residues: 1-810 <PET>

A;Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026 A;Experimental source: leukocyte; lung fibroblast R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Biochem. Blophys. Res. Commun. 173, 1013-1018, 1990 A;Title: Definition of the transcription initiation site of human plasminogen gene in A;Reference number: I52242; MUID:91097523

A;Status: translated from GB/EMBL/DDBJ A; Accession: I52242

A; Molecule type: DNA A; Residues: 1-16 <MAL1>

A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. FEBS Lett. 213, 254-260, 1987 R;Fitle: Molecular cloning and characterization of a full-length cDNA clone for human A;Reference number: A26466; MUID:87162490 A;Accession: A26646

A; Molecule type: mRNA
A; Residues: 1-471,'D',473-810 <FOR>
A; Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A; Experimental source: liver

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R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Blochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human
A;Reference number: 145961; MUID:85023311
A;Accession: I62738 A; Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA A;Residues: 292-471,'D',473-810 <MAL2> A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031

A; Status: translated from GB/EMBL/DDBJ A; Accession: 184609

A; Molecule type: DNA
A; Residues: 367-419 < MAL3>

A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111 R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, Eur. J. Blochem. 114, 465-470, 1981

A; Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

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R; Wiman,
Eur. J. E
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A; Residues: 483-507, 'E', 509-604 <WI3>
A; Residues: K.C.; Bernabe, P.; Arzadon, L.; Summaria,
J. Biol. Chem. 248, 1631-1633, 1973
A; Title: The primary structure of human plasminogen.
A; Reference number: A92125; MUID: 73149248
A; Contents: annotation; active Site
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A;Title: Primary structure of the B-chain
A;Reference number: A04627; MUID:77225245
A;Accession: A04627
                                                                                                                                                                                                                        R;Tulinsky, A.; Mulichak, A.M. submitted to the Brookhaven Protein Data Bank, A;Reference number: A51341; PDB:1PK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G. J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferatinal R;Reference number: A58811; MUID:97067211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-mainocarboxylic acid-binding sites
A;Reference number: A92382; MUID:82213905
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A;Accession: A04626
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A; Accession: A00929
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A; Accession: S03735
submitted to the Brookhaven Protein Data Bank, August 1993
A; Reference number: A51911; PDB:1PKR
                                                                                                            submitted to the Brookhaven Protein Data Bank, A; Reference number: A51488; PDB:2PK4
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A; Title: The fibrin-binding site of human plasminogen. Arginines 32 and A; Reference number: A92458; MUID:85054794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Contents: annotation; omega-aminocarboxylic acid binding sites R;Vall, Z.; Patthy, L. J. Biol. Chem. 259, 13690-13694, 1984
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A;Title: Studles on the active center of human A;Reference number: A92048; MUID:69234739
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Sottrup-Jensen, L.; Petersen
                                                                                                                                                                                                                                                                                                                                          Reference number: A58812; MUID:9548733
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                                                    T.P.; Tulinsky,
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Biochem. 50,
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A;Title: (1)H:NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: $43645; MUID:94237157
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmi A;Fitle: Solution structure of the epsilon-aminohexanoic acid complex of human plasmi A;Reference number: A58817; MUID:94237158
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKH
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                                                                  C;Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; F;1-96/Domain: plasminogen-related protein precursor homology <PLPH> F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibit C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial c C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin.
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A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen ac A;Reference number: A39483; MUID:92118803
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A; Title: Crystal and molecular structure of human plasminogen
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Biochemistry 30, 10576-10588, 1991
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                                         F; 20-810/Product: plasminogen #status experimental <PRO>
                                                                                                                                                                                               C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
                                                                                                                                                                                                                                                                      A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a sthe walls of the graafian follicle; also activates the urokinase-type plasminogen
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A; Introns: 17/1; 62/2; 98
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F;20-96/Domain: activation peptide #status experimental
                                                                                                                                                                                                                                         A; Pathway: fibrinolysis
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                                                                                                                                                                                                                                                                                                                                                                                                       98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-ray crystallography, 1.67 angstroms, residues 376-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ravichandran,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by (1)H-NMR, residues 103-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1 angstroms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.25 angstroms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.48 angstroms,
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            <APT>
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F;79-466/Product: angiostatin #status experimental <AST>
F;97-580,581-810/Product: plasmin #status experimental <MAT>
F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4/
F;481-560/Domain: kringle homology <KR5
F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R;Lijnen, H.R.; van Hoef, B; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076
A;Recession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LII>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin mediately after dissociation from the clot. In the presence of the inhibitor, the activate information involves also removal of the activation peptide.
C;Comment: Stromelysin I (see PIR:KCMSSI) acts on plasminogen to produce angiostatin. To effin solid timers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Characterization of the cDNA coding for mouse plasminogen and localization A;Reference number: A38514; MUID:91184812
A;Accession: A38514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Degen, S.J.F.; Bell,
Genomics 8, 49-61, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Pathway: fibrinolysis
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
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                                                          F;582-812/Domain: chain B #status predicted <BCH>F;582-805/Domain: trypsin homology <TRY>F;49-73,53-61,103-181.124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,33
                                                                                                                                                                          F:275-352/Domain: kringle homology <KR3>F:377-454/Domain: kringle homology <KR4>F:481-560/Domain: kringle homology <KR5>
                                                                                                                                                                                                                                                                                       F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                           F;20-96/Domain: activation peptide #status predicted <APT>F;79-466/Product: angiostatin #status predicted <AST>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vans the walls of the graafian follicle; also activates the urokinase-type plasminogen act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eful in treating solid tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                    F;97-581,582-812/Product: plasmin #status
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
                               bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                     97-581/Domain: chain A #status predicted
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F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Cj1467 [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni c;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000 C;Accession: B81293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and in vitro expression of A;Reference number: JQ1987; MUID:92300329 A;Accession: JQ1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical 8.5K protein - turkey rhinotracheitis virus (strain UK/3BV/85)
N;Alternate names: ORF 2 protein
C;Species: turkey rhinotracheitis virus
RESULT 5
S56296
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A; Residues: 1-73 < YUQ>
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A;Experimental source: serotype O2, strain NCTC 11168
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                                                                                                                                                                                                                            A;Gene: Cj1467
                                                                                                                                                                                                                                                    C; Genetics:
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A; Residues: 1-254 < PAR>
                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 403,
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210 RKIYDY 215
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les 6; Conserv
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5; Conserv
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5; Conser
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                                                                                                                                                          Conservative
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                                                                                                                                                                            94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                          Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB Pred. No. 8.6;
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                                                                                                                                                        Mismatches
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                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                              Length 254;
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                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.; Basham, D.;
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                                                                                                                                                              Gaps
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                                                                                                                                                              0,
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probable membrane protein YFR041c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein F018
C;Species: Saccharomyces cerevisiae

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Qγ
                                                                                                                                                                                                   A;Map position: 1
C;Superfamily: Vibrio cholerae probable transposase VC0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82355
                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004108; GB:AE003852; NID:g9654578; PIDN:AAF93361.1; GSPDB:GN00A;EXperimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-404 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A82035; MUID:20406833
A;Accession: D82355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transposase VC0185 [imported] - Vibrio cholerae (strain N16961 serogroup 01)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: dnaJ amino-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D44597; NID:g871938; PID:d1008597; PID:g871940
R;Eki, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Yeast 12, 149-167, 1996
A;Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome A;Reference number: S63787; MUID:96287652
A;Accession: S63788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;133-149/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;44-108/Domain: dnaJ amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:8-24/Domain: transmembrane #status predicted <TM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:D44597; NID:g871938; PID:d1008597; PID:g871940
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A; Residues: 1-295 < EKI>
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A; Accession: S62252
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A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Dec-1997 C;Accession: S56296; S62252; S63788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Murakami,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D50617; NID:g836685; PID:d1009921; PID:g836796; MIPS:YFR041c
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A; Residues: 1-295 <MUR>
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                                                                                                             Matches
                                                                                                                                                                 Query Match
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                                                                                                    Local Similarity es 5; Conserv
                                                1 RKLYDY 6
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                                                                                                       Conservative
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                                                                                                                              94.1%;
83.3%;
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83.3%;
                                                                                                    1; Mismatches
                                                                                                                              Pred. No. 49;
                                                                                                                                                        Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32;
Pred. No.
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                                                                                                                                                        DB 2;
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                                                                                                                                                     Length 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.J.
                               Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
A;Accession: E64358
                                                                                                                                                                                                                                                          C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: E64358
                                                                                                                                                           R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                     ribosomal protein L5 - Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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A; Map position: circular chromosome
                                                                                                                                                                                                                                                      A; Gene: AGR_C_723
                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                     A_rTitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A_rReference number: A_r7359; PMID:11743194 A_rRecession: A_r7409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: A97409
                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE007869; PIDN:AAK86226.1; PID:g15155328; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AGR_C_723 [imported] - Agrobacterium tumefaciens (strain C58, Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A42289
R;Kanagasundaram, V.; Scopes, R.K.
T. Bacteriol. 174, 1439-1447, 1439-1447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose-fructose oxidoreductase (EC 1.1.-.-) precursor - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: oxidoreductase
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 <math display="inline">A, Reference: A42289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M97379; NID:g155587; PIDN:AAA27690.1; PID:g155588
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A; Residues: 1-439 <KAN>
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129 RKVYDY 134
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                                                                                                                                       Local Similarity
                                                    1 RKLYDY 6
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                                                                                                         Conservative
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                                                                                                                                 91.2%;
83.3%;
                                                                                                         1;
                                                                                                                                    Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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Pred. No. 53;
                                                                                                      Mismatches
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                                                                                                                                                           Length 142;
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× 0

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C;Accession: S26824
R;Kuo, T.T.; Tan, M.S.; Su, M.T.; Yang, M.K.
Nucleic Acids Res. 19, 2498, 1991
A;Title: Complete nucleotide sequence of filamentous phage Cflc
A;Reference number: S26824; MUID:91252299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Du, Z.; Gattung, S. submitted to the BMBL Data Library, November 1996 submitted to the BMBL Data Library, November 1996 submitted to the BMBL Data Library, November 1996 submitted to the BMBL Data Library, November 1996
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                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-388 < KUO>
                                                                                                                                                                                                                                                                                                                           hypothetical protein - phage Cflc
C:Species: phage Cflc
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C:Accession: S26824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C01G8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T29261
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A; Residues: 1-190 <BUL>
A; Cross-references: GB:U67497; GB:L77117; NID:g2826284; PIDN:AAB98458.1; PID:g1591171;
                                                                                                                                                                A;Cross-references: EMBL:M57538; NID:g166169;
                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                       A; Accession: S26824
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 18/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: C01G8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-345 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z20597
A; Accession: T29261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: FOR415069-415641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                            Query Match
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     155
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                                                                                           Local
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                                       1 RKLYDY 6
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                                                                                                                                             the nucleotide sequence was submitted
     KKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conserv
                                                                                         Similarity
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     160
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                                                                        Conservative
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83.3%;
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Pred. No.
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Pred. No. 76;
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                                                                                                        DB 2;
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                                                                                                                                           to the EMBL Data
                                                                                                                                                              PIDN: AAA32201.1;
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                                                                      0;
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                                                                                                                                          Library, February 1991
                                                                                                                                                          PID:g166170
                                                                                                                                                                                                                                                                     from Xanthomonas campes
                                                                     0;
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A;Gene: S1
A;Genome: I
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: strain B31
R;Feng, S.; Das, S.; Lam, T.; Flavell, R.A.; Fikrig, E.
Infect. Immun. 63, 3459-3466, 1995
A;Title: A55-kilodalton antigen encoded by a gene on a
A;Reference number: 140296; MUID:95369900
A;Accession: 140296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
"---hes 5; Conserva
                                                                                                                                                                                                                                                                                                                                A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-18, 'R', 20-417 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: E70207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen S1 - Lyme disease spirochete plasmid A/1p54 (;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: E70207; I40296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SA1524
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: B89954
                                                                                                                                                                                                                                                                                  A; Experimental source: strain
                                                                                                                                                                                                                                                                                                        A; Cross-references:
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A; Residues: 1-417 <K
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Nature 390,
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A; Residues: 1-409 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000790; NID:g2690224; PIDN:AAC66229.1; PID:g2690228; TIGR:BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                  Matches
                                                                                                                                                Query Match
397 KKLYDY 402
                                                                                                                             Local
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                                                1 RKLYDY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.; Garland, S.
0, 580-586, 1997
                                                                                                                                                                                                     plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-417 <KLE>
                                                                                                  Similarity 5; Conserv
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83.3%;
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83.3%;
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82;
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80;
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phosphopyruvate hydratase (EC 4.2.1.11) [imported] - Streptococcus pneumoniae (strain R6 C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-oct-2001 #sequence_revision 22-oct-2001 #text_change 02-Nov-2001 C;Accession: D98001
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; F. e. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Appeliance of the Bacterium Streptococcus pneumoniae Strain R6.
A;Rocession: D98001
A;Accession: D9801
A;Status: preliminary
A, McConsolinary
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: B95130
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-434 < KUR>
A; Cross-references: GB: AE007317; PIDN: AAK99840.1; PID: g15458655; GSPDB: GN00174
C; Genetics:
A; Gene: eno
C; Superfamily: enolase
C; Keywords: carbon-oxygen lyase; hydro-lyase
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C;Superfamily: enolase
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A;Residues: 1-434 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75238.1; PID:g14972605; GSPDB:GN00164; TIGR:SP4
Search completed: November Job time: 10 secs
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253 RKVYDY 258
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83.3%;
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83.3%;
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    Mismatches

    Mismatches

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:34:41; Search time 30 Seconds (without alignments)
22.215 Million cell updates/sec

Title: US-09-657-431-11
Perfect score: 6
Sequence: 1 RKLYDY 6

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_032802:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT: *

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: *

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: *

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT: *

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *

11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

25: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

26: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

27: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

28: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

29: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

		,			SUMMARIES	
Result		% Query				
No.	Score	Match	Match Length DB	DB	ij	Description
_	6	100.0	6	18	AAW34302	Kringle 5 peptide
ν	6	100.0	6	21	AAB01903	Human plasminogen
ω	6	100.0	6	22	AAB92098	Laminin fragment S
4	თ	100.0	6	22	AAB36572	Mammalian kringle
S.	o	100.0	7	18	AAW34303	Kringle 5 peptide
δ	đ	100.0	7	18	AAW34304	Kringle 5 peptide
7	6	100.0	7	18	AAW34306	Kringle 5 peptide
æ	6	100.0	7	18	AAW34299	Kringle 5 peptide
9	6	100.0	7	18	AAW34290	Human kringle 5 pe
10	6	100.0	7	18	AAW34291	Human kringle 5 pe
11	6	100.0	7	21	AAB01888	Human plasminogen

7444444 64000000000000000000000000000000	114 115 116 117 118 119 119 120
6 100.0 6 100.0 7 100.0 8 100.0 9 100.0	100. 100. 100. 100. 100. 100.
111 112 112 112 112 112 112 112 112 112	
218 2118 2118 2118 2118 2118 2118 2118	
AAB92094 AAB36569 AAB36569 AAB36564 AAB36568 AAB36568 AAB36597 AAB3692090 AAB3692090 AAB3692090 AAB3601911 AAB0191914 AAY58668 AAB0191913 AAB0191913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913 AAB01913	AAB01889 AAB01900 AAB92097 AAB36571 AAB36571 AAB36579 AAB92101 AAB92101 AAB36575 AAB36575 AAB36575 AAB36575
Laminin fragment S Mammalian kringle Laminin fragment S Laminin fragment S Laminin fragment S Mammalian kringle Mammalian kringle Sequences flanking Kringle peptide #2 Laminin fragment S Mammalian kringle Laminin fragment S Laminin fragment S Laminin fragment S Mammalian kringle Human plasminogen	Human plasminogen Laminin fragment S Mammalian kringle Mammalian kringle Mammalian kringle Kringle peptide #1 Laminin fragment S Laminin fragment S Mammalian kringle Mammalian kringle Kringle 5 peptide Human plasminogen

ALIGNMENTS

PA PA	PR	PR	ΡF	×	y X X	PN	YY T	FΤ	H H	HH	XX	SO	××	KW.	X :	XX	KW.	X X	4 5	J >	Y DI	XX	AC X	RESU AAW3 ID
(ABBO) ABBOTT LAB.		03-APR-1997; 97US-0832087.	05-MAY-1997; 97WO-US07700.		13-NOV-1997	WO9741824-A2.	<pre>/note= "C-terminal amide"</pre>	Modified-site 6	modified site i /note= "N-Ac-Arg"	Key Location/Qualifiers		Synthetic.		kringle 5 receptor.	autoimmune disease: ocular disease: capillary proliferation; therapy;	psoriasis; arthritis; macular degeneration; diabetic retinopathy;	metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;	Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;	viingte a heberge iingment.	Kringle 5 pentide fragment	14-MAY-1998 (first entry)		AAW34302;	RESULT 1 AAW34302 ID AAW34302 standard; peptide; 6 AA.

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RESULT 2
AAB01903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc plasminogen. K5 peptide fragments homologous to this sequence, are carticularly primary or metastatic solid tumours, carcinomas, sarcomas, periodic fragments homologous to this sequence, are lymphomas, haemangiomas. They can also be used for treating or preventing cancer, cc lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The crapillary proliferation within atherosclerotic plaque, haemophiliac compiliary proliferation, ulcres etc., also as contraceptives that compiliary proliferation, ulcres etc., also as contraceptives that compiliary proliferation, ulcres etc., also as contraceptives that compiliary opinists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound capents. Antagonists may be used to induce angiogenesis, e.g. for wound capents. Antagonists and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their cresponse to the peptides or used for identification of smaller compiliary they have solotimes greater inhibitory against bovine capillary cells in vitro than kringle 1-4 peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
               05-MAY-1997;
                                                                                                                                                                                                                                                             Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiplicer; antipheumatic; antiarthritic;
                                                                               US6057122-A
                                                                                                                                  Modified-site
                                                                                                                                                                                                                      HOMO
                                                                                                                                                                                                                                                    antiangiogenic;
                                                                                                                                                                                                                                                                                                                                   Human plasminogen kringle 5 peptide fragment #9.
                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000
                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB01903 standard; peptide; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is synthetic a kringle 5 (K5) peptide homologous to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davidson DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RKLYDY 6
                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 45; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gubbins EJ,
              97US-0851350
                                                                                                                                                                                                                                                cancer; tumour; autoimmune disease.
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                             /note= "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                             "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18; 1
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 3
AAB92098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB018BB, AAB018BB, AAB018B, AAB018B
17-MAY-1999;
10-SEP-1999;
                                                                                   17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), coular diseases, skin diseases, skin diseases, rheumatoid arthritis), coular diseases, skin diseases.
                                                                                                                                                23-NOV-2000
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminin fragment SEQ ID NO:1274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB92098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB92098 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                      hydroxyl; thiol; hormone; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100–1:300, followed by incubating and isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of preparing plasminogen kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Column 37; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0643219.
97US-0832087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to C reactive group (II) active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids. CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic CC peptides are not suitable as drug candidates as they require frequent CC administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or CC life) and specificity as bonding to large molecules decreases. CC intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                    Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36572 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                      WO200070665-A2
                                                                                                                                                                                                                                                                                                                                                           Mammalian kringle 5 peptide SEQ ID NO:11
                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2001 (first entry)
(CONJ-) CONJUCHEM INC
                                 17-MAY-1999;
                                                                 17-MAY-2000; 2000WO-IB00763.
                                                                                                                                                                        Mammalia
                                                                                                                                                                                                     haemangioma; Kasposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0159783.
                                 99US-0134406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milner PG,
                                                                                                                                                                                                        sarcoma; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; I
6.4e+05;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to albumin prevents length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                        growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AAW34303
ID AAW
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RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           costeopathic activities, and is an angiogenesis inhibitor. (1) are useful costeopathic activities, and is an angiogenesis inhibitor. (1) are useful corrections. (1) are also useful for manufacturing a medicament extending the in vivo half-life of a kringle 5 peptide in a patient to provide an anti-angiogenic effect. In particular, a modified kringle 5 provide an anti-angiogenic effect. In particular, a modified kringle 5 correction in inflammation, chronic articular rheumatism or psoriasis), or considered with inappropriate or inopportune invasion of considered considered with inappropriate or inopportune invasion of considered considered considered in atherosclerotic plaques or osteoporosis), or concer associated disorders (e.g. solid tumours, solid tumour concernations), and considered considere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a modified anti-angiogenic peptide (1 comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood component to form stable covalent bonds. The reactive group is selected from succinimidyl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bridon
                                                                                                                                                                                                                                                                                                           plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
psoriasis; arthritis; macular degeneration; diabetic retinopathy;
autoimmune disease; ocular disease; capillary proliferation; therapy;
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                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kringle 5 peptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW34303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW34303 standard; peptide;
                                                                    Modified-site
                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                      kringle 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                             /note= "C-terminal amide"
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                                                                                                                                                                                         Location/Qualifiers
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Pred. No.
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6.4e+05;
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                                                                                            autoimmune d
kringle 5 r
                                                                                              Plasminogen; human; Kringle 5 peptide; anti-anglogenesis agent, constatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therap;
Modified-site
                                                         Synthetic
                                                                                                                                                                                                              Kringle 5 peptide fragment.
                                                                                                                                                                                                                                                       14-MAY-1998
                                                                                                                                                                                                                                                                                                                                 AAW34304 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1997;
03-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RKLYDY 7
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                                                                                            receptor.
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                     human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
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96US-0643219
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                  Location/Qualifiers
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Pred. No.
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. 6.4e+05;
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                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                            Matches
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metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy;
                               Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
                 metastatic solid tumour; carcinoma; sarcoma;
                                                                Kringle 5 peptide fragment.
                                                                                                     14-MAY-1998
                                                                                                                                                                   AAW34306 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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03-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, psoriasis, arthritis etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-558670/51
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6; Conserv
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                                                                                                  (first entry)
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Pred. No.
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thes 0;
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ID AAW3
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XXX
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                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, particularly primary or metastatic solid tumours, carcinomas, particularly primary prim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; ocular disease; capillary proliferation; therapy; kringle 5 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphomas, haemangiomas. They can also be used for treating or prevent psoriasis, arthritis, macular degeneration and diabetic retinopathy. fragments can also be used to treat autoimmune or ocular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is synthetic a kringle 5 (K5) peptide homologous to human
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96US-0643219.
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                                                                                   7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                 Score 6;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 DB 18; I 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                         Gaps
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Matches
                               Query Match
Best Local
                                                                                                                                                                                    joints, vound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis, arthritis, macular degeneration and diabetic retinopathy. fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atheroscleroic plaque, haemophiliac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is synthetic a kringle 5 (K5) peptide homologous to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davidson DJ,
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03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kringle 5 peptide fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 44; 78pp; English.
                                                                                                                                Sequence
6
                                  Similarity
                                                                                                                                7 AA;
Conservative
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96US-0643219
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                                  100.0%;
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                                  Score 6;
Pred. No.
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   Mismatches
                                  DB 18; 1
. 6.4e+05;
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1 RKLYDY 6 RKLYDY 7

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RESULT 9

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                                                                   Query Match
                                                                                                                                                                        (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantily the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capillary proliferation within atherosclerotic plaque, haemophiliac joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-anglogenesis agents, specifically for treating or preventing cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 62; Page 67; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
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03-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, psoriasis, arthritis etc.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragments can also be used to treat autoimmune or ocular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly primary or metastatic solid tumours, carcinomas, sarcomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                      Local
         Similarity 6; Conser
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      Conservative
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Pred. No.
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DB 18; 1
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hes 0;
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Typically they have 800-times greater inhibitory

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                                                                                                                                                                                                            particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac
           response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against
                                                                                joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wour healing. The K5 peptides are also used to raise specific antibodies for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their
                                                                                                                                                                                                                                                                                                  This sequence is a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer,
                                                                                                                                                                                                                                                                                                                                                                           Claim 62; Page 67; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                              New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davidson DJ,
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03-MAY-1996;
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                                                            endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumour and carcinomas of various organs such as breast, genital tract,
                                                                                                   The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
                                                                                                                                                                                                Preparation of Kringle five peptide fragment for treating various disorders such as anglogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                               03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anglogenesis; antiproliferative; antiarteriosclerotic; cyt
antipsoriatic; antiinflammatory; antiulcer; antirheumatic;
           diseases (e.g.,
                                               endocrine glands, skin, tumours of the brain and eyes and solid tumours
                                                                                                                                                                      Example 10; Column 38; 48pp; English.
                                                                                                                                                                                                                                                                                            Davidson DJ
                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          US6057122-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antianglogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB01888 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against bovine capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKLYDY
                                                                                                                                                                                                                                                                 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasminogen kringle 5-derived peptide,
psoriasis), blood vessel diseases
         from haematopoietic malignancies such as leukaemias and as. They are also used for the prophylaxis of various au s (e.g., rheumatoid arthritis), ocular diseases, skin di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; kringle 5 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                      LAB.
                                                                                                                                                                                                                                                                                                                                               96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                                                                                                                       97US-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; tumour; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "3-Iodotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells in vitro than kringle 1-4 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
(e.g. haemangiomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
            autoimmune
diseases
                                                                             tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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333333333<del>%</del>&
AAB01889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratt disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB011889, AAB01889, AAB01895-B01905 represent human plasminogen kringle 5-derived peptides synthesised and used in
                                                                                                                        Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthri
                                                                                                                                                                                                                                              03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                           WPI;
                                                                                                                                                                                                 Davidson DJ
                                                                                                                                                                                                                                                                                  05-MAY-1997;
                                                                                                                                                                                                                                                                                                        02-MAY-2000
                                                                                                                                                                                                                                                                                                                                 US6057122-A
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiangiogenic; cancer; tumour; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01889 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplifications
                                                                                                                 incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKLYDY
                                                                                                                                                                           2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen kringle 5-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                              96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                  97US-0851350
                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention
                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.
                                                                                                                                                                                                                                                                                                                                                       "3-Iodotyrosine; C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                              "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; I
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scratch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and plasmase in the ratio 1:100-1:300, rises mixing mammalian plasminogen and telastase in the ratio 1:100-1:300 are inhibitors of angiogenesis and the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours

and

various organs such as breast,

genital tract,

Example 11; Column 38; 48pp; English.

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                 Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                     03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AABO1888, AABO1889 and AABO1895-B01905 represent human plasminogen kringle 5-derived peptides synthesised and used in exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
                                                                                                                                                              WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                               05-MAY-1997;
                                                                                                                                                                                                                                                                                                                             02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                          US6057122-A
                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                       (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human plasminogen kringle 5 peptide fragment #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osier-Webber
                                                                                       involves mixing mammalian plasminogen incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB01900 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RKLYDY 6
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                                                                                                                                                                                           힏
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                    96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                               97us-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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The invention relates to a method of preparing peptide fragments. The method comprises mixing elastase in the ratio 1:100-1:300, followed by

plasminogen kringle 5 mammalian plasminogen and incubating and isolating

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently

amino/hydroxyl/thiol groups on blood

components

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6

Example 6; Column 36; 48pp; English.

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RESULT 14
AAB92097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the fragment. The kringle 5 peptides are inhibitors of angiogenesis and cendothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, carcinomas of various organs such as breast genital tract, carcinomas from haematopoletic malignancies such as leukaemias and carising from haematopoletic malignancies such as leukaemias and cymphomas. They are also used for the prophylaxis of various autoimmune chiefer (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber (c.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber (c.g., psoriasis), diseases caused by excessive or abnormal stimulation of cendothelial cells (e.g., Crohn's disease, atherosclerosis), diseases (which have angiogenesis as a pathologic consequence (e.g., cat scratch (c.g., cat ovulation and establishment of the placenta. CC sequences AAB01888, AAB01889 and AAB01895-B01905 represent human plasminogen kringle 5-derived peptides synthesised and used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                          Disclosure;
                                                                                                                                      Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                        WPI; 2001-112059/12
                                                                                                                                                                                                                       Bridon DP,
                                                                                                                                                                                                                                                                                    15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB92097 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                 17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB92097;
                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydroxyl; thiol; hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laminin fragment SEQ ID NO:1273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasminogen kringle 5-derived pept exemplifications of the invention.
                                                                                                                                                                                                                                                   (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RKLYDY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA;
                                                                                          Page 612;
                                                                                                                                                                                                                       Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                  99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                          733pp; English
                                                                                                                                                                                                                     Milner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 6;
Pred. No.
                                                                                                                                                                                                                       PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                       Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                      to albumin prevents length of in vivo a
                                                                                                                                                                                                                       Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                        vivo activity
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RESULT 15
AAB36571
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The present invention describes a modified anti-angiogenic peptide (I) comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood components to form stable covalent bonds. The reactive group is selected from succinimidyl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and osteopathic activities, and is an angiogenesis inhibitor. (I) are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; resortopic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; antiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia; haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
                                                                                                                                                                                                                                                                                                                                        New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                Claim 6; Page 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bridon DP, Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2000; 2000WO-IB00763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thibaudeau K, Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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6.4e+05;
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treating angiogenesis in a human,

where the derivative is reacted

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Search completed: November Job time: 30 secs
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                                                                                                                                                                                                                                                          CC with blood proteins. (I) are also useful for manufacturing a medicament CC extending the in vivo half-life of a kringle 5 peptide in a patient to CC provide an anti-angiogenic effect. In particular, a modified kringle 5 CC peptide can be used for treating inflammatory disorders (e.g. immune and Cn non-immune inflammation, chronic articular rheumatism or psoriasis), CC disorders associated with inappropriate or inopportune invasion of CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis, CC capillary proliferation in atherosclerotic plaques or osteoporosis), or CC cancer associated disorders (e.g. solid tumours, solid tumour CC metastases, angiofibronmas, retrolental fibroplasia, haemangiomas, CC Kasposi's sarcoma or other cancers requiring neovascularisation to CC support tumour growth). The peptides are useful for treating these CC diseases in mammalian or human patients. AAB36502 represents a mammalian CC kringle 5 protein, and AAB3653 to AAB36577 represent specifically vy
                                                                                                                                                                          Matches
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                          Sequence
                                                                                  1 RKLYDY 6
                                                                                                                               1 RKLYDY
                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                          7 AA;
                                                                                                                               6
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                      8
                    2002, 09:37:20
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Pred. No.
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6.4e+05;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21; Search time 17.6667 Seconds (without alignments) 37.723 Million cell updates/sec

Perfect score: US-09-657-431-11 34

1 RKLYDY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq_032802:*

1: /SIDSI/gcgdata/ge
2: /SIDSI/gcgdata/ge
3: /SIDSI/gcgdata/ge
3: /SIDSI/gcgdata/
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10: /SIDSI/gcgd
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14: /SIDSI/gcgd
15: /SIDSI/gcgd
16: /SIDSI/gcgd
17: /SIDSI/gcgd
18: /SIDSI/gcgd
19: /SIDSI/gcgd | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAB01888	AAW34291	AAW34290	AAW34299	AAW34306	AAW34304	AAW34303	AAB36572	AAB92098	AAB01903	AAW34302	ID	
Human plasminogen	Human kringle 5 pe	Human kringle 5 pe	Kringle 5 pentide	Kringle 5 peptide	Kringle 5 peptide	Kringle 5 peptide	Mammalian kringle	Laminin fragment S	Human plasminogen	Kringle 5 peptide	Description	

4	44	43	42	41	40	39	38	37	36	ω U	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
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21	18	21	21	21	21	21	21	18	22	22	22	22	22	22	21	22	22	22	22	22	22	21	18	22	22	22	22	22	22	22	22	21	21
AAB01890	AAW34286	AAB01916	AAB01913	AAB01917	AAY58868	AAB01914	AAB08413	AAW19256	AAB36565	AAB92095	AAB92090	AAB36570	AAB92096	AAB83293	AAB15521	AAB36568	AAB36564	AAB92093	AAB92089	AAB36569	AAB92094	AAB01899	AAW34298	AAB36575	AAB36567	AAB92101	AAB92092	AAB83292	AAB36576	AAB36571	AAB92097	AAB01900	AAB01889
plasminoge	_	_	_	_		plasi	_	Human plasminogen	an kringle		raqment	an kringle	fraqment	Œ			Mammalian kringle		ragment	ro -	Laminin fragment S	a			an kringl	fragment		eptide	Mammalian kringle		Laminin fragment S		Human plasminogen

ALIGNMENTS

RESULT 1 AAW34302

AAW34302 standard; peptide; 6 AA

AAW34302;

14-MAY-1998 (first entry)

Kringle 5 peptide fragment.

Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer; metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therapy; kringle 5 receptor.

Synthetic.

Modified-site Modified-site /note= "N-Ac-Arg" Location/Qualifiers

WO9741824-A2

/note= "C-terminal amide"

13-NOV-1997.

05-MAY-1997; 97WO-US07700

03-APR-1997; 03-MAY-1996; 97US-0832087 96US-0643219

(ABBO) ABBOTT LAB.

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RESULT 2
AAB01903
ID AAB0
XX AAB0
XX AAB0
XX Plas
XX Plas
KW Plas
KW Anti
KW Anti
XW Andi
FT Modi
FT Modi
FT Modi
FT WS6(
XX VS6(
XX V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc particularly primary or metastatic solid tumours, carcinomas, sarcomas, comparison of the pertial collar tumours, carcinomas, sarcomas, collar proposed collar provides and so be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac collar proliferation within atherosclerotic plaque, haemophiliac collar diseases, and capillary proliferation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or collar diseases, and establishment of the placenta. K5 antisera or collar diseases, and sease sease and collar diseases, e.g. for wound collar diseases, and for affinity purification of K5 receptors. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 corresponse to the peptides or used for identification of smaller antiagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively commal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is synthetic a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davidson DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-558670/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 45; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human plasminogen kringle 5 peptide fragment #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB01903 standard; peptide; 6 AA
                                      05-MAY-1997;
                                                                                                     02-MAY-2000.
                                                                                                                                                                       US6057122-A
                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                      97US-0851350
                                                                                                                                                                                                                                      /note= "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /note= "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang J;
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Pred. No. 6.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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17-MAY-1999; 10-SEP-1999; 17-MAY-2000; 23-NOV-2000 WO200069900-A2 Synthetic Homo sapiens hydroxyl; thiol;

99US-0134406 99US-0153406

2000WO-US13576.

component;

hormone; growth factor; neurotransmitter

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RESULT 3
AAB92098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and conditional cell proliferation and migration. The peptides are useful cc endothelial cell proliferation and migration. The peptides are useful cc for treating angiogenic diseases, primary and metastatic solid tumours can carcinomas of various organs such as breast, genital tract, can carcinomas of various organs such as breast, genital tract, conditional from haematopoletic malignancies such as leukaemias and clymphomas. They are also used for the prophylaxis of various autoimmune cc diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases cc (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber cc Syndrome), diseases caused by excessive or abnormal stimulation of conditional cells (e.g., Crohn's disease, atherosclerosis), diseases cubich have angiogenesis as a pathologic consequence (e.g., cat scratch cc agent which inhibits ovulation and establishment of the placenta. Cc sequences AAB01889, AAB01889 and AAB01895-B01905 represent human cc plasminogen kringle 5-derived peptides synthesised and used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of Kringle five peptide fragment for treating various disorders such as anglogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Column 37; 48pp; English.
                                                                                                                                                                                                                                      Protection; endogenous therapeutic peptide; peptidase; conjugation;
blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                      Laminin fragment SEQ ID NO:1274.
                                                                                                                                                                                                                                                                                                                            22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                AAB92098;
                                                                                                                                                                                                                                                                                                                                                                                                  AAB92098 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RKLYDY 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
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AAB36572
ID AAB36572
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XX O9-M
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XX O9-M
XX WASK
KW Krir
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KW VASK
KW Lapso
KW Canp
KW Capp
KW Capp
XX WASK
XX OPSO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a CC comprising a therapeutically active amino acid region (III) and a creative group (II) (e.g. succinimidyl and maleimido groups) attached to C reactive group (II) active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids. CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic CC peptides are not suitable as drug candidates as they require frequent CC administration due to rapid degradation by peptidases in the body. CC reduces the action of peptidases to increase length of activity (half CC intracellular mentals and interference with physical activity (half contention) and specificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 612;
                                                                                                                                                                                                                                                                                                                                                                                                                      Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36572 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                 WO200070665-A2
                                                                                                                                                                                                                                                                                                                              Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian kringle 5 peptide SEQ ID NO:11.
                                                                       17-MAY-1999;
                                                                                                                                    17-MAY-2000; 2000WO-IB00763.
                                                                                                                                                                                                                                                                                                                                                                                               haemangioma;
      (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and attaching therapeutic peptides degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Kasposi's
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                                                                       99US-0134406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     neovascularisation; tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to albumin prevents length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thibaudeau
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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CC groups. (I) can have anti-inflammatory, vasotropic, cytostatic, cytostatic, antipsoriatic, antidiabetic, antiarteriosclerotic and consteopathic activities, and is an angiogenesis inhibitor. (I) are useful contrasting angiogenesis in a human, where the derivative is reacted cytostatic and is an angiogenesis in the derivative is reacted cytostatic and is an angiogenesis in a human, where the derivative is reacted cytostatic and is an angiogenesis in a human, where the derivative is reacted cytostatic and is an anti-angiogenesis in a human, where the derivative is reacted cytostatic and is a second cytostatic and is reacted cytostatic and in a patient to cytostatic and in a patient in a patient
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PEN STATE THE STATE OF THE STAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 9; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastatic psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen; human; Kringle 5 peptide; anti-anglogenesis agent; cancer;
metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
psoriasis; arthritis; macular degeneration; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; ocular disease; capillary proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kringle 5 peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998 (first entry)
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                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kringle 5 receptor.
                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                              /note-
                                                                                                                                                    /note= "3-I-tyrosyl"
                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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                                                                              "C-terminal amide"
                                                                                                                                                                                                                                       "N-Ac-Pro"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 22;
Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contracting togenes is agency, specifically not interching the money, cancer, architecturing primary or metastatic solid tumours, carreinomas, sarcomas, companies, and also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The Crapillary proliferation within atherosclerotic plaque, haemophiliac compillary proliferation within atherosclerotic plaque, haemophiliac compillary proliferation within atherosclerotic plaque, haemophiliac compillary proliferation, ulcers etc., also as contraceptives that companies in an an establishment of the placenta. So antisera or compile compositions and establishment of the placenta. So antisera or compile composition of an establishment of the placenta. So antisera or composition and establishment of the placenta. So antisera or companies. Antagonists may be used to induce angiogenesis, e.g. for wound compile the solution of the proliferation and for affinity purification of K5 receptors. The K5 composition of the periodes (ab), composition of the periodes (ab) are used to detect/quantify the periodes in composition of smaller compositions. The Ab are used to detect/quantify the periodes in composition of smaller compositions and the substitution of smaller compositions. The K5 peptides (and K5 fusion proteins) selectively compositions and compositions and compositions and composition of smaller compositions and compositions and compositions and compositions are used to detect/quantify the peptides in commosition of smaller compositions and compositions and compositions and compositions are used to detect the composition of smaller compositions are used to detect the composition of smaller compositions and compositions are used to detect the composition of smaller compositions and compositions are used to detect the composition of smaller compositions are used to detect the composition of smaller compositions and compositions are used to detect the composition of smaller compositions are used to detect the composition of small
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Best Local :
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                                                                                                                          metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therap
Modified-site
                                                                      Synthetic
                                                                                                                                                                                                 Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent;
                                                                                                                                                                                                                                                         Kringle 5
                                                                                                                                                                                                                                                                                                       14-MAY-1998
                                                                                                                kringle 5 receptor.
                                                                                                                                                                                                                                                                                                                                                      AAW34304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy
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                                                                                                                                                                                                                                                      peptide fragment.
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Location/Qualifiers
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Pred. No. 6.4e+05
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                                                                                                                            capillary proliferation; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer; metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy;
                                                                                                       Kringle 5 peptide fragment.
                                                                                                                                                              14-MAY-1998
                                                                                                                                                                                                                                                           AAW34306 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page 45; 78pp; English.
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03-MAY-1996;
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96US-0643219
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Pred. No. 6.4e+05;
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RESULT 8
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                                                                                                                                                                                                                                                                                                          CC plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, cc particularly primary or metastatic solid tumours, carcinomas, sarcomas, cc lymphomas, haemangtomas. They can also be used for treating or preventing cp psoriasis, arthritis, macular degeneration and diabetic retinopathy. The cc psoriasis, arthritis, macular degeneration and diabetic retinopathy. The cc partial proliferation within atherosclerotic plaque, haemophiliac compiliary proliferation within atherosclerotic plaque, haemophiliac compiliary proliferation, ulcers etc., also as contraceptives that compiliar of plates, wound granulation, ulcers etc., also as contraceptives that compiliar of compiliar of compiliar of the placenta. K5 antisera or cc (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound cc agents. Antagonists may be used to induce angiogenesis, e.g. for wound cc agents and for affinity purification of K5 receptors. The K5 cr deeptors may then be expressed in tumour cells to increase their cc response to the peptides or used for identification of smaller cc antagonists. The Ab are used to detect/quantify the peptides in commal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
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                                                                                                                                                                                                            Matches
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                    AAW34299;
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nes 6; Conserv
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                                                                                                                                                                                                              Score 34; DB 18;
Pred. No. 6.4e+05;
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This sequence is synthetic a kringle 5 (K5) peptide homologous to human complaining the complete of the comple
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metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
psoriasis; arthritis; macular degeneration; diabetic retinopathy;
autoimmune disease; ocular disease; capillary proliferation; therapy;
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03-MAY-1996;
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                                                                                                                                Similarity
                                                                                                                                                                                                                                                                7 AA;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gubbins EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0832087.
96US-0643219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-Ac-Pro"
                                                                                                                           100.0%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
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                                                                                           Mismatches
                                                                                                                                         6.4e+05;
                                                                                                                                                                                       DB 18;
                                                                                                                                                                                  Length 7;
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RESULT 9

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2 RKLYDY

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AAW34290
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AC AAW3
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AC AAW3
AXX
DT 14-M
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A HUMMA
                                                                                                                                                                                 C capillary proliferation within atherosclerotic plaque, haemophiliac joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce anglogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in commandical samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothellal cells with low toxicity against cormal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 62; Page 67; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-558670/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
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03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW34290;
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                 Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis, arthritis etc., including gene therapy
                                                                                                                                               Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gubbins EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0832087
96US-0643219
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                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J;
Score 34; DB Lo;
Pred. No. 6.4e+05;
                                                                    Length 7;
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Matches

Conservative

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Indels

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                                                                                 anti-anglogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), receptors may then be expressed in tumour cells to increase their
normal cells. Typically they have 800-times greater inhibitory activity
               response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against
                                                                                                                                                                                                                                                                                                                          This sequence is a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence,
                                                                                                                                                                                                                                                                                                                                                                                   Claim 62; Page 67; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davidson DJ, Gubbins EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1997;
03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cance metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimmune disease; ocular disease; capillary proliferation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                     cancer, psoriasis, arthritis etc., including gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-558670/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW34291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 receptor.
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96US-0643219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _note= "optionally has nitrogen protecting group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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RESULT 11
AABO1888
ID AABO188
ID AA
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                      endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                           peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating elastase in the kringle 5 peptides are inhibitors of angiogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                        incubation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davidson DJ
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03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human plasminogen kringle 5-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-2000
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                                                                                                                                                                                                                                                                                         invention relates to a method of preparing plasminogen kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKLYDY 6
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                                                                                                                                                                                                                                                                                                                                                Column 38; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        isolation
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97US-0832087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "3-Iodotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-terminal acetyl moiety"
     vessel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells in vitro than kringle 1-4 peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain;
  diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4e+05;
(e.g. haemangiomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 12
AAB01889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which have angiogenesis as a pathologic consequence (e.g., cat scrat disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AABO1188, AABO1889 and AABO1895-BO1905 represent human plasminogen kringle 5-derived peptides synthesised and used in exemplifications of the invention.
                                                                                                                             Preparation of Kringle five peptide fragment for treating various disorders such as anglogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthri
                                                                                                                                                                                                                                                       03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Syndrome), diseases caused by excessive or abnormal stimulation endothelial cells (e.g., Crohn's disease, atherosclerosis), dise
                                                                                                                                                                                WPI; 2000-349573/30.
                                                                                                                                                                                                        Davidson DJ
                                                                                                                                                                                                                               (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                            05-MAY-1997;
                                                                                                                                                                                                                                                                                                                   02-MAY-2000
                                                                                                                                                                                                                                                                                                                                           US6057122-A
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiangiogenic; cancer; tumour; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB01889 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RKLYDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasminogen kringle 5-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                LAB
                                                                                                                                                                                                                                                       96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                           97US-0851350
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /note= "3-Iodotyrosine; C-terminal amide moiety"
                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                         "N-terminal acetyl moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cat scratch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen an elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful

Example 11; Column 38; 48pp; English

incubation and isolation

and carcinomas

for treating angiogenic diseases,

of various organs such as breast, genital tract

primary and metastatic solid

tumours

and

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RRESULT 13
AABO10
IID AABO10
XXX AABO10
XXX BABO2
XXX Huma
XXX Plas
KW anti
KW anti
KW anti
KW anti
XXX Home
OS Home
O
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                                                                                                                                                                                      Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen; human; kringle 5 domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                         WPI; 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                     Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human plasminogen kringle 5 peptide fragment #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB01900 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endocrine glands, skin, tumours of the brain and eyes and solid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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nes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKLYDY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0643219.
97US-0832087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97us-0851350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating

bonds with amino/hydroxyl/thiol

groups on blood components to

covalently

Example 6; Column 36; 48pp; English.

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RESULT 14
AAB92097
DЬ
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Best Local
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                                                                                                                                                                                                                                                                                                 17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human plasminogen kringle 5-derived peptides synthesised and used in exemplifications of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract,
             The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleinido groups) attached a less therapeutically active amino acid region (IV), which covalently
                                                                                                                                               Modifying and attaching therapeutic peptides peptidase degradation, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB92097 standard; Peptide; 7 AA
                                                                                                Disclosure;
                                                                                                                                                                                                   WPI; 2001-112059/12
                                                                                                                                                                                                                                 Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laminin fragment SEQ ID NO:1273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB92097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                 (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RKLYDY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                Page 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                               99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                733pp; English.
                                                                                                                                                                                                                                    Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                   increasing length
                                                                                                                                                                                                                                  Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                 to albumin length of
                                                                                                                                                                                                                                    Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                   n prevents
in vivo a
                                                                                                                                                   vivo activity
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   The present invention describes a modified anti-angiogenic peptide (I) comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood components to form stable covalent bonds. The reactive group is selected from succinimidyl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antinheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and osteopathic activities, and is an angiogenesis inhibitor. (I) are useful
                                                                                                                                                          Claim 6; Page 9; 82pp; English.
                                                                                                                                                                                       New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                         WPI; 2001-090970/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                 (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2000; 2000WO-IB00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200070665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian kringle 5 peptide SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36571 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RKLYDY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA;
                                                                                                                                                                                                                                                                                                          Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                    99US-0134406
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                                                                                                                                                                                                                                                                                                      Thibaudeau K, Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 22;
. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
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angiogenesis in a human,

where the derivative is reacted

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Search completed: November Job time: 18.6667 secs
                                                                                     B
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                   metastases, angiofibromas, retrolental fibroplasia, haemangiomas, Kasposi's sarcoma or other cancers requiring neovascularisation to support tumour growth). The peptides are useful for treating these diseases in mammalian or human patients. AAB36562 represents a mammalian kringle 5 protein, and AAB36563 to AAB36577 represent specifically claimed kringle 5 peptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with blood proteins. (I) are also useful for manufacturing a medicament extending the in vivo half-life of a kringle 5 peptide in a patient to provide an anti-anglogenic effect. In particular, a modified kringle 5 peptide can be used for treating inflammatory disorders (e.g. immune and non-immune inflammation, chronic articular rheumatism or psoriasis),
                                                                                                                                                                                                                                                                                                                                                                                                                             disorders associated with inappropriate or inopportune invasion of vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques or osteoporosis),
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           cancer associated disorders (e.g. solid tumours, solid tumour
                                                                                                                                                                                       Local Similarity
                                                                                     1 RKLYDY 6
                                                                                                                          1 RKLYDY 6
                                                                                                                                                               6;
                                                                                                                                                                                                                                                  7 AA;
                                                                                                                                                                   Conservative
                                                                                                                                                                                   100.0%;
                   8
                   2002, 09:34:52
                                                                                                                                                                 0;
                                                                                                                                                                            Score 34; DB 22;
Pred. No. 6.4e+05;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                      Length 7;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:22; Search time 28.6667 Seconds (without alignments) 72.416 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-657-431-5 75 1 RNPDGDVGGPWK 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : sp_archea:*
sp_bacteria:* sp_invertebrate:*

SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungd:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_virus:*
13: sp_virus:*
13: sp_virus:*
14: sp_unclass
15: sp_archeap
17: sp_archeap sp_organelle:*
sp_phage:*
sp_plant:*
sp_rotent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_mammal:*
sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	o	5	4	ω	N	ᆫ	Result No.
52	52	52	52	52	53	55	56	56	58	64	64	64	64	70	70	Score
69.3	69.3	69.3	69.3	69.3	70.7	73.3	74.7	74.7	77.3	85.3	85.3	85.3	85.3	93.3	93.3	Query Match Length
211	210	208	109	75	710	709	716	716	806	812	812	648	567	810	334	
11	4	4	6	6	13	13	11	11	δ	11	11	4	4	4	6	DB
055027	Q13494	Q9BYM0	Q9N1B8	Q9BGN9	Q91402	Q90ZN6	Q91XG8	P70521	018783	Q91WJ5	Q9R0W3	Q9H1V4	Q13208	Q15146	046507	ID
7 mus	Q13494 homo sapien	Q9bym0 homo sapien	Q9n1b8 ovis aries	Q9bgn9 bos taurus	Q91402 xenopus. he	Q90zn6 brachydanio	Q91xg8 mus musculu	P70521 rattus norv	018783 macropus eu	Q91wj5 mus musculu	Q9r0w3 rattus norv	Q9h1v4 homo sapien	Q13208 homo sapien	Q15146 homo sapien	046507 papio hamad	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
44	45	45	45	45.5	•	46	46	47	47	47	47.5	47.5	47.5	47.5	47.5	47.5	48	48	48	49	50	50	50	50	52	52	52	52
•	60.0	60.0		-		•	61.3	62.7	62.7	62.7	63.3	63.3	63.3	63.3	63.3	63.3	64.0	64.0	64.0	65.3	66.7	66.7	66.7	66.7	69.3	69.3	69.3	69.3
522	608	607	140	420	399	312	260	420	385	382	492	473	473	473	452	117	717	263	263	215	716	704	313	111	728	726	296	290
10	13	13	11	4	4	4	16	13	υ	13	4	11	11	4	13	4	13	4	4	13	13	13	13	σ	6	13	4	4
Q9LIW0	Q9PTW7	Q91001	Q9D874	Q9BTP9	Q96GL8	09NSV1	Q57371	Q90504	Q25101	Q90WT4	80M960	Q924S4	Q99N43	Q9BY70	064060	Q9UGS5	P70006	Q96FE7	000318	042341	Q91691	Q90865	Q9PU78	077688	Q9BH09	Q90978	Q14519	Q02935
Q9liw0 oryza sativ				Q9btp9 homo sapien	Q96gl8 homo sapien	homo	_		Q25101 herdmania m	Q90wt4 crocodylus	Q96mu8 homo sapien	Q924s4 rattus norv	Q99n43 mus musculu	Q9by70 homo sapien	Q90y90 xenopus lae	Q9ugs5 homo sapien	P70006 xenopus lae		000318 homo sapien	_	Q91691 xenopus lae		Q9pu78 crocodylus	077688 oryctolagus		Q90978 gallus gall	Q14519 homo sapien	Q02935 homo sapien

ALIGNMENTS

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SQ
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Best Local Similarity
                                       Matches
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                                                                                                                    PFAM; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRPSIN.

PRINTS; PR007128; KRINGLE.

SMART; SM00130; KR; 5.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00021; KRINGLE 1; 5.

PROSITE; PS50070; KRINGLE 2; 5.

PROSITE; PS500134; TRYPSIN_DOM; 1.

PROSITE; PS500135; TRYPSIN_SER; 1.

PROSITE; PS500135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q15146 PRELIMINARY;
Q15146;
Q15046; Tremblrel 0
01-NOV-1996 (Tremblrel 0
01-DEC-2001 (Tremblrel 0
PLASMINOGEN PRECURSOR.
                                                                                                                                                                                                                                                          InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                SEQUENCE
                                                                                                Hydrolase; Serine protease; Signal.

STGNAT. 1 19 POTENTIAL.
                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                    Browne M.J., Chapman C.G., Mitchell D., Robinson J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                       Fibrinolysis 0:0-0(1991)
                                                                                                                                                                                                                                                                                                                                                               "Expression of recombinant human
HeLa cells.";
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
532
                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO PEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
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                  1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RNPDGDVGGPW 11
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RNPDGDVGGPW 542
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                                                                                                                                                                                                                                                                                                              P00747; 2PK4
                                                                                                                                                                                                                                       PF00024; PAN;
                                                                                                                                                                                                                                                PF00051; kringle;
                                                                                                                                                                                                                                                                                                                       M74220; AAA36451.1;
                                                                                                                                                                                                                                             ; IPR001314; Chymotrypsin.
; IPR000001; Kringle.
; IPR003014; PAN.
; IPR003609; Pan_app.
; IPR001254; Trypsin.
; O0051; kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                              20
810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 AA;
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                                       Conservative
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90555
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100.0%;
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01,
19,
                                                                               MW;
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                                     0;
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                               Score 70;
Pred. No.
                                                                           PLASMINOGEN.
; B05C7D4B0D020B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C7DC06E03B965286 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           Ι.,
                                     Mismatches
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                                               DB 4;
0.0048;
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0.0019;
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                                                                                                                                                                                                                                                                                                                                           ALSO KNOWN AS
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                                                                                                                                                                                                                                                                                                                                                                       aglycoplasminogen
                                    0;
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                                    Gaps
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RESULT Q13208

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RESULT
Q9H1V4
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                                                                Q9H1V4;
                                        InterPro;
InterPro;
                                                                                                                                                                                                     SEQUENCE FROM N.A. Bird C.;
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ1182A14.3 (SIMILAR TO MST1 (MACROPHAGE STIMULATING 1 (HEPATOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q13208 PRELIMINARY; PRT; 567 AA. Q13208; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                      DJ1182A14.3.
                                                                                                                                                                                                                                                                                                                                                                                       GROWTH FACTOR-LIKE))).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00130; KR; 4.

SMART; SM00473; PAN_BA; 1.

PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003509; Pan_ai
InterPro; IPR001254; Tryps:
Pfam; PF00051; kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20191171; PubMed=10728827;
Degen S.J.F., McDowell S.A., Waltz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
InterPro;
                       InterPro;
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U28054; AAC63092.1;
HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Seq. 8:409-413(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  like protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of the human D1F15S1A locus: a chromosome 1 locus with 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity to the chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDGDPGGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Œ
                     ; IPR001314; (; IPR000001; ); IPR003014; |
IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease. 567 AA; 64117 MW; 3FC38B07F1645810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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Trypsin.
                                      Chymotrypsin.
Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.3%;
90.9%;
Pan_app
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kringle
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                                                                                                                                                        EMBL/GenBank/DDBJ databases.
PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 4;
Pred. No. 0.031;
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                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding for hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local
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01-MAY-2000 (TIEMBLIEL 13, Created)

01-MAY-2000 (TIEMBLIEL 13, Last sequence update)

01-DEC-2001 (TIEMBLIEL 19, Last annotation update)

PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS000021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
Hydrolase; Serine Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
Pfam; PF00
                                                                                                                                                                                                                                                                                                                                                                                            Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9R0W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
                                                                                                                                                                                                                        EMBL; AJ242649; CAB46014.1; HSSP; P00747; 1PMK. MEROPS; S01.233; -.
                                                                                                                                                                                                                                                                           receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                           PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00018; KRINGLE.
                                                                                                    Pfam; PF00051; kringle; 5. Pfam; PF00024; PAN; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                         InterPro; IPR003609; Pan_app.
InterPro; IPR001400; SOMATOTROPIN.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                          Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis
                                                                                                                                                                                                                                                                                                                                           MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                         TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                       InterPro; IPR003609;
                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                TRYPSIN FAMILY.
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                                                                                                                                                                                      IPR003014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.3%;
90.9%;
                                                                                                                                                                                     PAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812
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RESULT 7
018783
ID 018783
ID 0187
AC 0187
DT 01-7
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ENAC
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Q91WJ5
ID Q91W
ID Q91W
AC Q91
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Best Local S
Matches 10
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Best Local
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O18783;
O1-JAN-1998 (TrEMBLrel. 05, 0
O1-JAN-1998 (TrEMBLrel. 05, I
O1-DEC-2001 (TrEMBLrel. 19, I
PLASMINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014773; AAH14773.1; -
EMBL; BC014773; AAH14773.1; -
SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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PROSITE; PS00134; TRYPSIN_HIS; UNKN
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal.
SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                       Lawn R.M., Schwartz K., Patthy L.;
"Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98004511; PubMed=9342350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9315;
                                           InterPro;
                                                                          InterPro;
                                                                                                                     MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 RNPDGDVNGPW 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 RNPDGDVNGPW 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                TRYPSIN FAMILY
                                                                                                                                                 AF012297; AAB65760.1; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
   IPR001314; Chymotrypsin. IPR000001; Kringle. IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812
90535 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASMINOGEN.
; 8C703C51410EBC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 11
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT
P70521
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Best Local
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SMART; SM00473; PAN, AP; 1.

SMART; SM00473; PAN, AP; 1.

SMART; SM00202; TYPP_SPC; 1.

PROSITE; PS00021; KRINGLE 1; 5.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50244; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                      SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease; Signal.
                                                                                                                                               InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P70521:
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
MACROPHAGE STIMULATING PROTEIN PRECURSOR.
  SEQUENCE
                                                                                                            SMART;
                                                                                                                      PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                          MEROPS; S01.975;
                                                                                                                                                                                                                                                                      EMBL; X95096; CAA64473.1; -. HSSP; P00747; 1KRN.
                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 227:273-280(1996).
                                                                                                                                                                                                                                                                                                             Takasu N., Suda T.;

Takasu N., Suda T.;

"Molecular cloning of Rat Macrophage-stimulating protein involvement in the Male Reproductive System.", involvement in the Male Reproductive System.", involvement in the Male Reproductive System.", and involvement in the Male Reproductive System." and involvement in the Male Reproductive System System (No. 1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97011126; PubMed-8858136; Ohshiro K., Iwama A., Matsuno K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003609; Pa
InterPro; IPR001254; Tr
InterPro; IPR00051; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P70521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527
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                                                                                                                                                                                                                                                                                                 TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDGDPNGPW 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNPDGDVGGPW
                                                                                                            SM00130; KR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
  716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease.
806 AA; 90981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
  AA;
  80733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58;
Pred. No.
06B7DF3EF56D921F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95FAA86DC20064D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Ezaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 AA.
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T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .42;
                                                                                                                                                                                                                                                                                                                                                                          Sakamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                       0.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                                                                                                                                                                                       Hamaguchi
                                                                                                                                                                                                                                                                                                                                                its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Q91XG8
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                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                                          Query Match
Best Local :
                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                       SEQUENCE FROM N.A.

Bassett D.I., Wilson S.W.;

Bassett D.I., Wilson S.W.;

"Early expression of zebrafish Hepatocyte Growth Factor-Like

"Early expression of zebrafish Hepatocyte Growth Factor-Like

suggests a conserved role in vertebrate neural induction.";

submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF370035; AAK54207.1; -.
                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                               01-DEC-2001 (TERMBLrel. 19, Created)
01-DEC-2001 (TERMBLrel. 19, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE 1.
                                                                                                                                                                                                                                                                                                  Q90ZN6;
01-DEC-2001
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC010551; AAH10551.1; - SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;
 422
                                                                                                                                                                                                                                                      HGFL1
                                                                                                                                                                                                                                                                                                                            Q90ZN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HEPATOCYTE GROWTH FACTOR-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91xG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91XG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       429 RNPDGDSHGPW 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 9; Conserv
             1 RNPDGDVGGPW
                                                                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNPDGDVGGPW
RNPDGDHHGPW 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPDGDSHGPW 439
                                              9;
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                             709 AA;
                                              Conservative
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                      11
                                                                                             81271 MW;
                                                          73.3%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             74.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.7%;
81.8%;
                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                          Score 55; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                            9907236C5DB73A20 CRC64;
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                           709
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0.78;
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1.78;
                                                                     DΒ
                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 716;
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                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                  Length 709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                               Ostariophysi;
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT Q91402

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Q9BGN
Q9BGN
Q9BGN
AC Q9BGN
DT 01-JUI
DT 01-DE
DE HEPAT
GN HGF
C Eukar
OC Eukar
OC Mamma
OC Mouma
OC NCBI
I RN [1]
RP SEQUE
RA OKUGA
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                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91402 PRELIMINARY;
Q91402;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-DEC-2001 (TrEMBLrel. 19, L
HEPATOCYTE GROWTH FACTOR.
                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
"Expression and action of hepatocyte growth factor
                    Okuda K.
                              Murakami S.,
                                           SEQUENCE FROM N.A.
TISSUE-UTERUS;
                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                               Q9BGN9
                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP, 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00021; KRINGLE_1; 3.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                  Q9BGN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                               165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001254; Trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003014;
InterPro; IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S77422; AAB34354.2; -. HSSP; P14210; 1BHT. MEROPS; S01.976; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus early embryogenesis.";
Mech. Dev. 49:123-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular cloning of Xenopus HGF cDNA and its expression studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95267690; PubMed=7748783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN FAMIL
                                                                                                                                                                                                                                                                                            RNPKGEEGGPW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00051; kringle; 4.
                                                                                             Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                           Serine protease.
710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                     Fujiwara C., Miyamoto Y., Takeuchi S., Takahashi S.,
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                        70.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan_app.
                                                                                                                                                                                                                                                                                                                                                        Score 53; 1
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                          75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 710 AA.
                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 710;
 in bovine
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                                                                                                                                                              RESULT 14
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Q9N1B8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT DR FT FT
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local
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     01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                        Q9BYMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000001; Kringle PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Reprod. 62:1844-1850(
EMBL; AF213397; AAF25945.1;
HSSP; P14210; 2HGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20297031; PubMed=10819791; Chen C., Spencer T.E., Bazer F.W.; "Expression of hepatocyte growth fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ovine uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9N1B8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=ENDOMETRIUM FROM DAY 1 CYCLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000001; Kringle.
InterPro; IPR00366; Prothrombin.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
SMART; SM00130; KR; 2.
PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
PROSITE; PS00020; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endometrial stromal and epithelial cells in vitro."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB056447; Hab333031.1; -. HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                      67 RNPRGEEGGPW 77
                                                                                                                                                                                                                                                                                  1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RNPRGEEGGPW 14
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 109
109 AA;
                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 AA; 8831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62:1844-1850(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                                                                    12501 MW; 1F88FE5DBC0D4A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                   69.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.3%;
72.7%;
       . 17, Created)
. 17, Last sequ
. 19, Last anno
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                            Score 52; DB 6
Pred. No. 0.46;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    829EEEFCC49701B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor and its receptor c-met in the
                                                                                                       208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA.
                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovoidea;
                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                         0;
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RESULT 15
013494
ID 01349
AC 01349
AC 01349
AC 01349
AC 01-NC
DT 01-NC
DT 01-NC
DT 01-NC
DE HGF
OS HGM
OC EUKA
OC MAMMI
OX NCBJ
RN [1]
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RN [1]
RN [1]
RN MED
RA GIO
RA MED
RA GIO
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q13494 PRELIMINARY;
Q13494;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-JUN-2001 (TrEMBLrel. 17, L
HGF AGONIST/ANTAGONIST.
                                          InterPro; IPR003609; Pan_app.
pfam; PF00051; Kringle; 1.
pfam; PF00024; PAN; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 30:9170-9176(1991).
EMBL; M75971; AAG53459.1; JOINED.
EMBL; M75967; AAG53459.1; JOINED.
EMBL; M75966; AAG53459.1; JOINED.
EMBL; M75968; AAG53459.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0018; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M75969; AAG53459.1; JOINED.
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEPATOCYTE GROWTH FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human hepatocyte growth factor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miyazawa K., Kitamura A., Kitamura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91369928; PubMed=1832556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=96278713; PubMed=8662798;

Gloce V., Csaky K.G., Chan A.M.L., Bottaro D.P., Taylor W.G.,

Jensen R., Aaronson S.A., Rubin J.S.;

Jensen R., Aaronson S.A., Rubin J.S.;

Hepatocyte growth factor (HGF)/NK1 is a naturally occurring

"Hepatocyte factor variant with partial agonist/antagonist activity.";

HGF/Scatter factor variant with partial agonist/antagonist activity.";

J. Biol. Chem. 271:3310-13115(1996).
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InterPro; IPR003966; Prothrombin.
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SEQUENCE 210 AA; 24116 MW; 94A6EE9C50DE5A86 CRC64;
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Sequence: OM protein - protein search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Database : Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Searched: PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* US-09-657-431-5 75 283138 segs, 96089334 residues November 8, 2002, 09:33:36; Search time 18 Seconds (without alignments) 64.060 Million cell updates/sec 1 RNPDGDVGGPWK 12 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. 283138

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W. Biochemistry 23, 4243-4250, 1984 A; Title: Characterization of a complementary deoxyribonucleic A; Reference number: I45961; MUID:85023311 A; Accession: I62738 A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 292-471, 'D', 473-810 <mal2> A; Cross-references: GB:KO2922; NID:g190112; PIDN:AAA60124.1; IA; Cross-references: GB:KO2922; NID:g190112; PIDN:AAA60124.1; IA; Cross-references: GB:KO2921; NID:g190110; PIDN:AAA60123.1; IA; R:Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Eur. J. Biochem, 114, 465-470, 1981 A; Title: Comparison of the primary structure of the N-termina</mal2>	Biochem. Biophys. Res. Commun. 1/3, 1013-1016, 1290 A;Title: Definition of the transcription initiation A;Reference number: I52242; MUID:91097523 A;Accession: I52242 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-16 cMALI> A;Residues: 1-16 cMALI> A;Residues: 1-16 cMALI> A;Residues: 1-16 cMALI> A;Rorsgren, M; Raden, B; Israelsson, M; Larsson, FBBS Lett. 213, 254-260, 1987 A;Title: Molecular cloning and characterization of A;Reference number: A26646; MUID:87162490 A;Accession: A26646 A;Molecule type: mRNA A;Residues: 1-471,'D',473-810 <for> A;Cross:references: GB:X05199; NID:g35530; PIDN:CAA A;Cross:references: GB:X05199; NID:g35530; PIDN:CAA</for>	RESULT 1 PLHU PLHU plasmin (EC 3.4.21.7) precursor [validated] - human plasmin (EC 3.4.21.7) precursor [misnomer] N;Alternate names: plasminogen precursor [misnomer] N;Alternate names: plasminogen precursor [misnomer] N;Contains: angiostatin; microplasmin; plasminogen C;Species: Homo sapiens (man) C;Species: Homo sapiens R;Petreson; T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. N;Petreson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. N;Petreson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. R;Petreson number: A35229; MUID:90202879 A;Accession: A35229; MUID:90202879 A;Rolecule type; DNA A;Residues: 1-810 <pet> A;Coss-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; A;Experimental source: Leukocyte; lung fibroblast R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candaani, G.; Meroni, G.; O</pet>	34 35 36 37 38 44 41 53
Malinowski, D.P.: ochemistry 23, 42 Title: Characteri Title: Characteri Reference number: Accession: I62738 Status: translate Molecule type: mR Residues: 292-471 Cross-references: Accession: I84609 Status: translate Molecule type: DN Residues: 367-419 Cross-references: Brunisholz, R.A.; Ir. J. Biochem. 11 Title: Comparison	Biophy Definition: It ion: It it trans le trype le referen Molecu Molecu Molecu Molecu Mijon: A	ate nam nas: ange s: Homo 24-Apr 24-Apr Cham. R. Charac	444 11. 444433 557
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E; Davie, E.W. 84 B4 Complementary deoxyribonucleion (1985023311) MBL/DDBJ 0 <malz> NID:9190112; PIDN:AAA60124.1; MBL/DDBJ MBL/DDBJ NID:9190110; PIDN:AAA60123.1; Schaller, J.; Rickll, E.E.; 1981 1981 mary structure of the N-termin</malz>	mun. 1/3, 1013-1016, 1390 transcription initiation site of hu ; MUID:91097523 GB/EMBL/DDBJ 890; NID:9190092; PIDN:AAA36454.1; P Israelsson, M.; Larsson, K.; Heden, 987 and characterization of a full-leng ; MUID:87182490 810 <for> 810 <for> 810 <for> 9179; NID:935530; PIDN:CAA28831.1; PI</for></for></for>	[validated] - human recursor [misnomer] smin; plasminogen smin; plasminogen semin; plasminogen plasminogen, A.; Davie, pg0 gene for human plasm:90202879	139 901 901 520 652 664 664 672 272 320 029 941 UT
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PIDN:AAA60124.1; PIDN:AAA60123.1; Fickli, E.E.; of the N-termin	28 2 23 25	tted] - human r [misnomer] plasminogen 02-Dec-1994 #text_change 15-Sep-2000 22738; I84609; \$03735; A00929; A04627; 35e, A.; Davie, E.W. or human plasminogen, a key proenzyme 379 76; NID:g190064; PIDN:AAA60113.1; PID: fibroblast	
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submitted to the Brookhaven Protein Data Bank, August 1993 A;Reference number: A51911; PDB:1PKR
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A,Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential A,Reference number: A92458; MUID:85054794
A,Gontents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site A,Gontents: annotation; fibrin binding site; Marti, D.; Soehndel, S.; McCance, S.G., R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.,
                                                                                                                                           A; Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Brookhaven Protein Data Bank, July 1991 A; Reference number: A51341; PDB:1PK4
                                                                                                                                                                                                            A;Reference number: A51488; PDB:2PK4
                                                                                                                                                                                                                                                       submitted to the Brookhaven Protein Data Bank, July 1991
                                                                                                                                                                                                                                                                                                                       R; Tulinsky, A.; Wu, T.P.
                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation; X-ray crystallography, 1.9 angstroms,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D. Biochemistry 37, 4699-4702, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cao, Y., Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G. J. Biol. Chem. 271, 29461-29467, 1996
A;Tille: Kringle domains of human angiostatin. Characterization of the anti-proliferation of the ant
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R;VOII; Z.; Patthy, L.
T Biol. Chem. 259, 13690-13694, 1984
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A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen A;Reference number: A92382; MUID:82213905
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A;Accession: A04626
A;Molecule type: protein
A;Residues: 483-507,'E',509-604 <WI3>
R;Robbins, K.C.; Bernabe, P; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
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A;Contents: annotation; active site
R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
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A;Accession: A04625
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A;Title: Primary structure of the B-chain
A;Reference number: A04627; MUID:77225245
A;Accession: A04627
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A;Accession: A00929
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J. Biochem. 58, 539-547, 1975
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J. Biochem. 50, 489-494, 1975
                                                                                                           Tulinsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W.R.; Summaria, L.; Robbins, K.C. em. 244, 3590-3597, 1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,51-71,'E',73-85,87-100 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73-76 <BRU>
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                                                                                                                                                                                                                                                                                                                                                             residues 376-454
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d PIR:FGHUGB).

C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately C:Comment: Plasmin is formed by alpha-2-antiplasmin (see PIR:ITHUA2) immediately rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibit C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial c C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin.
F;20-96/Domain: activation peptide #status experimental <APT>
                                           F;20-810/Product: plasminogen #status experimental <PRO>
                                                                             C;Reywords: angiogenesis inhibitor; blood; duplication; fibrinolysis F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                  C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
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R;Rejante, M.R.; Lilnas, M.

Eur. J. Biochem. 221, 939-949, 1994

A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmi A;Reference number: A588L7; MUID:94237158
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
                                                                                                                                                                                                                                                                                     ns the walls of the graafian follicle; also activates the urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                      A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 6q26-6q27
A; Introns: 17/1; 62/2; 98
                                                                                                                                                                                                                                                                        A; Pathway:
                                                                                                                                                                                                                                                                                                                                                                                             C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:119498; OMIM:173350
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Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157
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R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at A;Reference number: A39483; MUID:92118803
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A; Contents: annotation; conformation by (1)H-NMR, residues 103-181
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A;Reference number: A65803; PDB:1HPJ
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Biochemistry 30, 10589-10594, 1991
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A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181 R; Padmanabhan, K.; Tulinsky, A.
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                                                                                                                                                                                                                                                               fibrinolysis
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                                                                                                                                                                                                                                                                                                                            dissolves the fibrin of blood clots; acts as a proteolytic factor in
                                                                                                                                                                                                                                                                                                                                                                                                              98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conformation by (1)H-NMR, residues 103-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1 angstroms, residues 102-181
                                                                                                                                                                fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues 377-454
                                                                                                                                                                glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR:UKH
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plasmin (EC 3.4.21.7) precursor - rhesus macaque
C; Species: Macaca mulatta (rhesus macaque)
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C; Accession: B32869; B30848
R; Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor - horse (f. N;Alternate names: plasminogen N;Contains: miniplasminogen C;Species: Equus caballus (domestic horse) C;Date: 28-Oct-1994 #sequence_revision 01-C;Accession: A61545; $17527 R;Schaller, J; Rickli, E.E. Enzyme 40, 63-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Rhesus monkey apollopprotein(a). Sequence, evolution, and sites of synt A;Reference number: A32869; MUID:89174660
A;Recession: B32869
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-810 <TOM>
A;Residues: 1-810 <TOM>
A;Residues: 1-810 <TOM>
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor C;Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-97Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;103-181/Domain: kringle homology <KR1>
   A;Title: Structural aspects of the plasminogen A;Reference number: A61545; MUID:89005015 A;Accession: A61545
A;Molecule type: protein A;Residues: 1-33;34-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:97-580,581-810/Product: plasmin #status experimental <MAT>
F:97-580/Domain: plasmin chain A #status experimental <CHA>
F:103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:377-454/Domain: kringle homology <KR3>
F:481-560/Domain: kringle homology <KR4>
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F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
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F;481-560/Domain: kringle homology <KR5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;79-466/Product: angiostatin *status experimental <AST> F;97-580,581-810/Product: plasmin *status experimental <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s: #status predicted
,665,760/Active site: His,
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Straub, C.; Kaempfer, U.; Rickli, E.E.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 70;
100.0%; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  horse (fragments)
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                                                                                                                                                                                                                                                               01-Nov-1996 #text_change 18-Jul-1997
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0.0018;
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                                                                                                                                                    of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 810;
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A47136

macrophage-stimulating protein 1 precursor - human

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 118-455 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C;Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F;1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <APT>
F;34-117,118-255,226-455/Product: plasmin (fragments) #status experimental <MAT>
F;37-114/Domain: kringle homology <KR4>
F;118-455/Product: miniplasminogen #status experimental <MIN>
F;126-205/Domain: kringle homology <KR5>
F;226-445/Domain: kringle homology <KR5>
F;226-445/Domain: trypsin homology <TRY>
F;226-445/Domain: trypsin homology <TRY>
F;267,310,405/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase F;1-37,38-117,118-460/Product: plasminogen. (fragments) #status experimental <PRO> F;1-37/Domain: activation peptide (fragment) #status experimental <APT> F;38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT> F;41-118/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-37;38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995
A;Accession: S28200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Structural aspects of the plasminogen of various species A;Reference number: A61545; MUID:89005015
A;Accession: B61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999 C;Accession: B61345; S28200 R:Schaller T. mith: 2
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A;Title: Complete amino acid sequence of equine miniplasminogen.
A;Reference number: S17527; MUID:92052077
A;Accession: S17527
B
                                                                                                                                                                                                                                    F;272,315,410/Active site: His, Asp,
                                                                                                                                                                                                                                                             F;118-460/Product: miniplasminogen #status experimental <MIN>F;132-211/Domain: kringle homology <KR5>F;236-460/Domain: plasmin chain B #status experimental <BCH>F;231-453/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Contains: miniplasminogen
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Enzyme 40, 63-69,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmin (EC 3.4.21.7) precursor -
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Best Local
                                                                                                                  Matches
                                                                                                                                                                         Query Match
   183
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                                                                                                               Local Similarity es 10; Conserv
                                                          1 RNPDGDVGGPW 11
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63-69, 1988
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                                                                                                                  Conservative
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   193
                                                                                                                                              85.3%;
90.9%;
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90.9%;
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Pred. No. 0.0095;
                                                                                                                                                 Pred. No. 0
                                                                                                                                                                         Score 64;
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                                                                                                                  Mismatches
                                                                                                                                                                                                                                 Ser #status predicted
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                                                                                                                                                                      Length 460;
                                                                                                                  Indels
                                                                                                                  0;
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                                                                                                                  Gaps
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N;Contains: angiostatin; plasminogen C;Species: Mus musculus (house mouse) C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999 C;Accession: A38514; S48202; S48203 R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W. Genomics 8, 49-61, 1990 fthe cDNA coding for mouse plasminogen and local A;Title: Characterization of the cDNA coding for mouse plasminogen and local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Rocess..... A; Rocess..... A; Rocess..... A; Rocess..... A; Rolecule type: mRNA A; Rolecule type: mRNA A; Rolecule type: mRNA A; Rolecules: 1-12, CC', 14-622, 'F', 624-711 < YOS> A; Rosidues: 1-12, CC', 14-622, 'F', 624-711 < YOS> A; Rosidues: 1-12, CC', 14-622, 'F', 624-711 < YOS> A; Rote: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this A; Note: authors translated the codon TTT for residue 623 as Leu; parts of this 
                                                                                                         A; Reference number: A38514; MUID:91184812
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F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F:110-186/Domain: kringle homology <KKR1>
F:191-268/Domain: kringle homology <KK2>
F:283-361/Domain: kringle homology <KK3>
F:370-448/Domain: kringle homology <KK4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:128833; OMIN:142408
A;Map position: 3p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma F;1-18/Domain: signal sequence #status predicted <SIG> F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M74178; NID:g183976; PIDN:AAA50165.1; PID:g183977
R;YOShImura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A;Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MSA;Reference number: A47136; MUID:93340141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
C; Date: 03-May-1994 #sequence_
C; Accession: A40331; B40331; A
                                                             A; Accession: A38514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmin (EC 3.4.21.7) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Macrophage stimulating protein: purification, partial amino acid sequence, and A; Reference number: A61395; MUID:91217635 A; Accession: A61395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Characterization of the DNF15S2 locus on human chromosome A;Reference number: A40331; MUID:92002016
A;Accession: A40331
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;484-711/Domain: beta chain #status_predicted <BCH>
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A; Residues: 1-711 <HAl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A47136
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A; Residues: 1-711 <HA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPW 11
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90.9%;
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                                                                                                                                                           for mouse plasminogen and localization of
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E.J.
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A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related protein
C; Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis;
F; 1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 1-19/Domain: signal sequence #status predicted <SIG>
                                                                             A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963 A;Experimental source: liver
                                                                                                                                                                                                                                                A; Reference number: S45046
A; Accession: S45046
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
C;Accession: $45046; A25835; I45961; S03736
C;Accession: $45046; A25835; I45961; S03736
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F;97-681/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;381-560/Domain: kringle homology <KR5>
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A;Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A; Note: it is uncertain whether Met-1 or Met-8 R; Schaller, J.; Moser, P.W.; Dannegger-Muller,
                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-812 <BER>
                                                                                                                                                                                                                                                                                                                                 A; Description: Cloning and characterizatin of the bovine plasminogen cDNA.
                                                                                                                                                                                                                                                                                                                                                                        R; Berglund, L.; Andersen, M.D.; Petersen, T.E. submitted to the EMBL Data Library, May 1994
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F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
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A; Residues: 20-25 <LIJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmin (EC 3.4.21.7) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;624,667,762/Active site: His, Asp, Ser #status predicted
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Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B #status predicted <BCH>
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90.9%;
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Pred. No. 0.018;
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                                      is the initiator
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    S.J.; Kampfer,
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A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related p
C; Superfamily: plasmin; kringle homology; plasminogen-related p
C; Keywords: duplication; fibrinolysis; glycoprotein; hydrolase;
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 1-26/Domain: plasminogen-related protein precursor homology
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A;Residues: 706-743, "4, "745-812 <MAL>
A;Residues: 706-743, "4, "745-812 <MAL>
A;Residues: 706-743, "4, "745-812 <AMAL>
A;Residues: 706-743, "4, "745-812 <AMAL>
A;Residues: 706-743, "10:g163551; PIDN:AAA30714.1; PID:g163552
A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
A;Brunlsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUID:81212097
A;Accession: S03736
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a value of the military of the molecular protein a value of the military of the m
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A;Title: Complete amino acid sequence of bovine plasminogen. C
A;Reference number: A25835; MUID:85203906
A;Accession: A25835
A;Molecule type: protein
A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic
A;Reference number: 145961; MUID:85023311
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F;485-564/Domain: kringle homology <KR5>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,
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A; Molecule type: mRNA
A; Residues: 1-4548 < MCI>
A; Cross-references: GB: X06290; EMBL: X06696; NID: g28619; PIDN: CAA29618.1; PID: g28620
R; Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn,
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
                                                                                                                                                                                                                                                                     A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen A;Reference number: S00657; MUID:88039109
A;Accession: S00657
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C; Species: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 330,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; McLean,
                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Homo sapiens (man)
;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000;
;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000;
;Accession: 800657; A28017; A47277; I66906; A47233; I52415; I65286;
;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless;
fature 330, 132-137, 1987
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90.9%;
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Pred. No.
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C:Superfamily: apolipoprotein(a); kringle homology; trypsin homolog
C:Superfamily: apolipoprotein(b); kringle homology; trypsin homolog
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homolog
C:Superfamily: apolipoprotein(b); kringle; lipid binding; lipoprotein(b); kringle; homology; kringle; kringle; lipid binding; lipoprotein(b); kringle; k
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Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome
A;Reference number: A47233; MUID:93087573
A;Accession: I60906
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X',4396-4401 
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A;Note: apo(a) gene 1 (nomenclature of
A;Accession: I65286
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A; Residues: 20-21, 'p', 23-34; 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200; 292-314, 'W', 316
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A; Note: several genes closely linked on chromosome 6 are identical in
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A; Residues: 1-16 < RE3>
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A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated A;Reference number: I52415, MUID:92207924
A;Accession: I52415
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A; Residues: 1-16 <RE5>
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A; Residues: 1-16 < RE2>
                                                                                                               F;1624-1701/Domain:
F;1738-1815/Domain:
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kringle homology <KR11>
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plasmin (EC 3.4.21.7) precursor - pig (fragment)
W;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
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C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
                                                                                                                                                                         Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmin (EC 3.4.21.7) precursor - western European hedgehog
C:Species: Erinaceus europaeus (western European hedgehog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46260
                                                                                                                        RESULT 10
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A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot A;Reference number: I46259; MUID:96025778
A;Accession: I46260
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F;4328-4541/Domain:
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F;4124-4201/Domain:
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F;2194-2271/Domain:
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0; Mismatches
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0.16;
                                                                                                                                                                                                                                                                      Length 810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.E.; Wade, D.P.; Byrne, C.D.; Fong
                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                      Gaps
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RiDegen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatcoyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
C;Accession: A40332; B40332
                                                                A; Molecule type: mRNA
A; Residues: 1-18, 'P',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a ns the walls of the graafian follicle; also activates the urokinase-type plasminogen A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol C;Keywords: fibrinolysis; glycoprotein; hydrolase_kidney; kringle; plasma; serine pr
C; Genetics:
                        A; Cross-references: GB: M74181; NID: g193833; PIDN: AAA50167.1; PID: g193834
                                                                                                                                A; Cross-references: A; Accession: B40332
                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-716 < DEG>
                                                                                                                                                                                                                                                                       A;Reterence number: A40332; MUID:92002017 A;Accession: A40332
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F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
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F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
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F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: krigsted kingles brooklogy (Fragment)
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Eur. J. Blochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;602,645,740/Active site: His, Asp, Ser #status predicted
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A;Tille: Comparison of the primary structure of the N-terminal CNBr fragments of huma A;Reference number: S03735; MUID:81212097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Function:
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                                                                                                                                                                GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
                                                                ,20-716 <DEG2>
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81.8%;
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A; Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1;

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thrombin (EC 3.4.21.5) precursor - bovine (Species: Bos primigenius taurus (cattle) C:Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999 C:Accession: S02537; A00915; A37552; 146045; S67518 R:Irwin, D.M.: Robertson, K.A.; MacGillivray, R.T.A. J. Mol. Biol. 200, 31-45, 1988 A;Title: Structure and evolution of the bovine prothrombin gene. A:Reference number: S02537; MUID:88245190 A;Accession: S02537
A;Status: not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:x95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C;Keywords: duplication; glycoprotein; growth factor; kringle F;1-31/Domain: signal sequence #status predicted <SIG> F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <ACH> F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH> F;110-186/Domain: kringle homology <KRII> F;110-186/Domain: kringle homology <KRII
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A; Residues: 1-716 <OHS>
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A;Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in A;Reference number: JC5061; MUID:97011126
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
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F:110-186/Domain: kringle homology <KR1>
F:191-268/Domain: kringle homology <KR2>
F:292-370/Domain: kringle homology <KR3>
F:379-457/Domain: kringle homology <KR4>
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379-457/Domain: kringle homology <KRI4>
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
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Matches
                                                                   Query Match
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Rosidues: 466-599, 'N', 501-625 < MA2>
A; Cross-references: EMBL: V00135; NID: 9772; PIDN: CAA23451.1; PID: 9808945
R; Pejler, G.; Karlstroem, A.R.; Berg, L.
R; Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Biochem. 227, 102-107, 1995
A; Title: Identification of the proteolytic thrombin fragments formed after cleavage w
A; Reference number: S67518; MUID: 95154277
A; Accession: S67518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent interaction with the negatively charged phospholipid membrane surface. C;Comment: The prothrombin precursor is synthesized in the liver. C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; processed blood coagulation; proc
                                                                                                                 F;367-616/Domain: trypsin homology <TRY>
F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;61,-66,91-104,109-187,130-170,188-182,214-292,235-275,263-287,339-485,394-410,539-55
                                                                                                                                                                                                                                                                                                                                                                                                                            F;109-187/Domain: kringle homology <KR1>
F;200-317/Domain: activation peptide 2 #status experimental <FR2>
F;214-292/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi tivation peptide and cleaves the remaining part into light and heavy chains. The acti
                                                                                                                                                                                                                                                                                                           F;318-366/Product: thrombin light chain *status experimental <LCH>F;367-625/Product: thrombin heavy chain *status experimental <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;25-43/Domain: propeptide #status predicted <PRO>F;28-88/Domain: Gla domain homology <GLA>
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A.Contents: annotation; residues 44-317, X-ray crystallography, R.Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A. Biochemistry 24, 6854-6861, 1985
F;409,465,571/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;44-199/Domain: activation peptide 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;44-625/Product: prothrombin #status experimental <MPT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 318-325;333-338, 'X', 340;367-374;481-484, 'X', 486-488;515-522 <PEJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Contents: annotation; gene structure R;MacGillIvray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980 A;Title: Cloning and analysis of a cDNA coding for bovine prothrombin. A;Reference number: I46045; MUID:81054926 A;Accession: I46045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Park, C.H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the evidence for 231-Ser is Scrowy
A;Note: disulfide bonds and carbohydrate binding sites were determined
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A;Title: Characterization of bovine prothrombin mRNA and its translation product. A;Reference number: A00915; MUID:84203525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 44-287, 'N',289-352, 'E',354,'Q',356-548,'ND',551-599,'N',601-625 <WAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: 600-Asn was also found R; Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
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A; Residues: 1-230, 'H', 232-625 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A00915
                                                           120,144,419/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #status experimental <FR1>
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Local

Similarity 8; Conserv

Conservative

73.3%; 72.7%;

Pred. No. 0.4; Score 55; Mismatches

DB 1;

Length 625;

0;

Gaps

0,

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A, Description: stimulates mitosis of hepatocytes and other cells
A, Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F; 42-477,478-709/product: hepatocyte growth factor #status predicted <ACH>
F; 115-193/Domain: kringle homology <KR1>
F; 115-193/Domain: kringle homology <KR2>
F; 198-275/Domain: kringle homology <KR2>
F; 375-453/Domain: kringle homology <KR4>
F; 375-453/Domain: kringle homology <KR4>
F; 478-709/Domain: kringle homology <KR4>
F; 478-709/Domain: kringle homology <KR4>
F; 478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F; 478-700/Domain: trypsin homology <TRY>
F; 521,212,281,322,379,550,637,666/Bindding site: carbohydrate (Asn) (covalent) #status predicted
F; 470-588/Disulfide bonds: #status predicted
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C; Accession: 151283
R; Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
wanh Dev. 49, 123-131, 1995
                                                                                                                                                                                                                                                                                                                                                                                             hepatocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Jate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51285
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard Development 121, 813-824, 1995
A;Title: A role for HGFVSF in neural induction and its expression in Hensen's node during A; Reference number: I51285; MUID:95237013
A;Accession: I51285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatocyte growth factor precursor - clawed frog
N;Alternate names: hepapoietin A; scatter factor
C;Species: Xenopus sp. (clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
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Best Local Similarity
Change 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues; 1-710 <NAK>
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A; Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
A; Reference number: I51283; MUID:95267690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
Query Match
Best Local Similarity
Best Acches 8; Conserve
                                                                                                                                                  A;Cross-references: GB:S77480; NID:g998675; PID:g998676
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F:124-197/Domain: kringle homology <KRG>
F;202-279/Domain: kringle homology <KR2>
F;296-374/Domain: kringle homology <KR3>
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                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-411 <STR>
                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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72.7%;
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72.7%;
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                                                          Score 52; DB 2; Pred. No. 0.79;
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Qy 1 RNPDGDVGGPW 11
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Db 169 RNPRGEEGGPW 179
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Search completed: November 8, 2002, 09:36:44
Job time: 19 secs



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21; Search time 9.33333 Seconds (without alignments) 49.782 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-657-431-5 75 1 RNPDGDVGGPWK 12

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29 30 31 33 33	22222 225 24 25 26	1 3 3 4 4 4 6 6 7 7 7 11 11 11 11 11 11 11 11 11 11 11	Result
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SEQUENCE OF 483-604. MEDLINE=76043692; PubMed=126863; Wiman B., Wallen P.;	SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810. Sottrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.; (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.); Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209, Raven Press, New York (1978).	SEQUENCE OF 20-100. SEQUENCE OF 20-100. MEDLINE-75093329, PubMed-122932; Wiman B., Wallen P.; Wiman B., Wallen P.; Structural relationship between 'glutamic acid' and 'lysine' forms of human plasminogen and their interaction with the NH2-terminal activation peptide as studied by affinity chromatography."; Eur. J. Biochem. 50:489-494(1975).	SEQUENCE OF 292-810 FROM N.A. SEQUENCE OF 292-810 FROM N.A. MEDLINE-85023311; PubMed-6148961; Malinowski D.F., Sadler J.E., Davie E.W.; "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen."; Biochemistry 23:4243-4250(1984).	SEQUENCE OF 20-810. SEQUENCE OF 20-810. Sottrup-Jensen L., Petersen T.E., Magnusson S.; Submitted (JUL-1977) to the PIR data bank.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-87162490; PubMed-3030813; MEDLINE-87162490; PubMed-3030813; FORSGren M., Raden B., Israelsson M., Larsson K., Heden LO.; "Molecular cloning and characterization of a full-length cDNA clone for human plasminogen."; FEBS Lett. 213:254-260(1987).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=90202879; PubMed=2318848; Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.; Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.; "Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system."; J. Biol. Chem. 265:6104-6111(1990).	Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	UL-19 AR-19 CT-20 minog	

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CARBOHYDRATE-LINKAGE SITE 268.
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Pirie-Shepherd S.R., Stevens R.D.
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"Structure of the omega-aminoca
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plasminogen ":
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MEDLINE=92031502; PubMed=1657148;
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J. BIOL. Chem. 264:5957-5965(1989).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE—TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND WON WILLEBRAND FACTOR.

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FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.

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FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN Z CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN Z CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

FINILARITY: BELONGS TO PEPTIDASE FAMILY. S1; ALSO KNOWN AS THE TRYESIN FAMILY. PLASMINGEN SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P12545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLMN_MACMU
                                                                                                                                                                          PIR; B30848; B30848.
PIR; B32869; B32869.
                                                                                                                                                                                                                                              use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
                                                                                    InterPro; IPR001314;
InterPro; IPR000001;
InterPro; IPR003014;
                                                                                                                                                                                                             EMBL; J04697; AAA36901.1;
                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Rhesus
                                                                                                                                           MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in lifted and this statement is not removed. Usage by and for contified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPDGDVGGPW 542
PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monkey apolipoprotein(a). Sequence, evolution, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 12, Created)
(Rel. 12, Last sequence up
(Rel. 40, Last annotation
precursor (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                          1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                    Chymotrypsin.
Kringle.
PAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 AA.
                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; L
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Best Local
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SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50134; TRYPSIN_HIS; 1.
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    532
                   RNPDGDVGGPW 11
  RNPDGDVGGPW
                                                                                 Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00722; CHYMOTRYPSIN
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124
152
185
188
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760
136
158
172
432
445
134
                                                                                    Conservative
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  542
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; Blood coagulation; Kringle; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810
580
810
810
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1181
1262
352
352
352
454
454
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454
1136
665
760
1136
1136
1172
                                                                                                                                                                                                                                                     90255
                                                                                                     93.3%;
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                                                                                                                                                             BY SIMILARITY.
BY SIM
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                 Score 70; DB; Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMEGA-AMINOCARBOXYLIC
OMEGA-AMINOCARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMEGA-AMINOCARBOXYLIC OMEGA-AMINOCARBOXYLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASMIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGHT CHAIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kringle;
                                                                                                       DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORM OF CHAIN
                                                                                                                           Length 810
                                                                                      Indels
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ACIDS.
ACIDS.
ACIDS.
ACIDS.
                                                                                    0;
                                                                                      Gaps
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RESULT 3
PLMN_CANFA

PLMN_CANFA

STANDARD;

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Pfam; PF00089; trypsin; 1.

SMART; SM00130; KR; 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS500240; TRYPSIN_DOM; 1.
                                          SITE
SITE
                                                                                               ACT_SITE
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01-NOV-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
 SEQUENCE
                                                                                                                           DISULFID
                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90175323; PubMed=2626424;
Schaller J., Straub C., Kaempfer U., Rickli E.E.;
"Complete amino acid sequence of canine miniplasminogen.";
Protein Seq. Data Anal. 2:445-450(1989).
                                                                                  ACT_SITE
                                                                                                                                                      DISULFID
                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                    Tissue
                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN P; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE WALKS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES TOKKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND YON WILLEBRAND FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEGIN SEQ. DATA ANAL. 2:445-450(1989).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: PLASMIN IS INACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUI FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00051; kringle;
                                                                                                                                                                                                                                                                                                                 remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000001;
IPR001254;
 333
                                                                                                                                                                                                                                                                                                                                Serine
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(Rel.
(Rel.
(EC 3.
                                                                                                          254
54
54
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130
145
279
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 AA;
                                                                                                                                                                                                                                                                                                              protease; Plasma; Glycoprotein; Fibrinolysis;
    Blood coagulation; Kringle; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20, Created)
20, Last sequence update)
40, Last annotation update)
.4.21.7) (Fragment).
                                                                                                                                                                                                        103
333
333
333
78
 36678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kringle.
Trypsin.
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 ¥;
                      INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).
                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                         PLASMIN
PLASMIN
               (BY SIMILARITY)
                                                                                                                                                                                                                                   SERINE PROTEASE.
BY SIMILARITY.
                                                                                                                                                                                                                                                               KRINGLE
C8C0271B6C6AC8D4 CRC64;
                                                                                                                                                                                                                                                            N HEAVY CHAIN
N LIGHT CHAIN
E 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY ALPHA-2-ANTIPLASMIN
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PLMN_HORSE
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Best Local
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DISULFID
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P80010;
01-NOV-1991
01-NOV-1991
16-OCT-2001
                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                             PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
SPO0021; KRIMGLE_1; 1.
PROSITE; PS50070; KRIMGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92052077; PubMed-1946332;
Schaller J., Straub C., Kaempfer U., Rickli E.E.;
"Complete amino acid sequence of equine miniplasminogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00051; kringle; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.233; -.
    DISULFID
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000001;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S17527; S17527.
HSSP; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                          Tissue
                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EATHLIN AND YON WILLEBRAND FACTOR.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEIN SEG. Data Anal. 4:69-74(1991).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT MEAKENS THE WALLS OF THE GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPDGDVNGPW 65
                                                                                                                                                                                                                                                                     remodeling;
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40, Last annotation update)
.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                            protease;
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90.9%;
                                                                                                                                                                                                                                                                     coagulation;
                                                                                                                                                                                                                                                                   Plasma; Glycoprotein; Fibrinolysis; agulation; Kringle; Zymogen.
INTERCHAIN (BY INTERCHAIN (BY BY SIMILARITY.
BY SIMILARITY.
                                                                                   SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                    PLASMIN HEAVY CHAIN PLASMIN LIGHT CHAIN
                                                                                                                                                                                  KRINGLE 5.
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                                            SIMILARITY).
SIMILARITY).
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RESULT 5
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AS Schaller J., Straub C., Kampfer U., Rickli E.E.,;

AT "Complete amino acid sequence of ovine miniplasminogen.";

AT Protein Seq. Data Anal. 5:21-25(1992).

C -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTECLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN AS CI AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS CI AND C.5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

C -I- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN AND TO PLASMIN BY PLASMINOGEN AND TO PLASMIN BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

-I- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                 InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
SMART; SM00130; KR; 1.
SMART; SM00130; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P81286;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00747; 5HPG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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                          Tissue remodeling;
                                                    Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS
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                                               Serine protease; Plasma; Glycoprotein; Fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                          Blood coagulation;
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90.9%;
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BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                             LEAST
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                        2 KRINGLE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 AA
                       Kringle; Zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 338;
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(See http://www.isb-sib.ch/announce/

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Best Local
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                      YOShimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
"Cloning, sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3.";
J. Biol. Chem. 268:15461-15468(1993).
-i- FUNCTION: PROBABLY HAS NO PROTEDLYTIC ACTIVITY, SINCE CRUCIAL AA CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P26927; Q13350; Q14870;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage stimulating protein).
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ACT_SITE
                                                                                                                                                                                   HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES -- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92002016; PubMed=1655021;
Han S., Stuart L.A., Friezner Degen S.J.;
"Characterization of the DNF15S2 locus on human chromosome 3: identification of a gene coding for four kringle domains with homology to hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
                                                                                                                                                                                                                           -!- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93340141; PubMed=8393443;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 30:9768-9780(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Kringle; Glycoprotein; Serine pro
                                                  BOVIN
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SM00473;
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                 Q28162;
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711 AA;
(Rel. 06, Created)
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                                  STANDARD;
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90.9%;
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KRINGLE 2.

KRINGLE 4.

SERIME PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.
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C -> F
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Y -> C.
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01-NOV-1997
16-OCT-2001
Plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88185329; PubMed-3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
"The N- and O-linked carbohydrate chains of human, bovine and
EMBL; X79402; CAA55939.1; -.
EMBL; K02935; AAA30714.1; -.
PIR; A25835; PLBO.
HSSP; P00747; 2PK4.
MEROPS; S01.233; -.
                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of a complementary deoxyribonucleic human and bovine plasminogen."; Biochemistry 23:4243-4250(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLG.
Bos taurus (Bovine).
                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          This
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"Cloning and
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                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fucosylation patterns.";
Eur. J. Biochem. 173:57-63(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete amino acid sequence of bovine plasminogen. Comparison with
                                                                                                                                                                                                                                                                            TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=3846532;
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 5.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                         P20918;
01-FEB-1991
01-FEB-1991
16-OCT-2001
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  Genomics [2]
                    SEQUENCE FROM N.A.

MEDLINE=91184812; PubMed=2081600;

Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;

Pegen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;

"Characterization of the cDNA coding for mouse plasminogen localization of the gene to mouse chromosome 17.";

Genomics 8:49-61(1990).
                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
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SIGNAL 1
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InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 5.
                                                                                                                                                                                                                                                                                     Plasminogen
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IPR000001; Kringle.
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(Rel. 17, Last sequence)
(Rel. 40, Last annotation)
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90.9%;
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KRINGLE 2.
KRINGLE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 1; Pred. No. 0.0075;
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                                                                                                                             CHAIN
CHAIN
                                                                                                                                                                                                                                                       SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 5.
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MEROPS; S01.233; -.
MGD; MGI:97620; Plg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           suppression of metastases by a Lewis lung carcinoma. ^n; Cell 79:315-328(1994).
                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00051; kringle; 5. Pfam; PF00024; PAN; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                       PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                 Tissue
                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANBOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TENDERN TAKENTY OF THE MALTER ACTIVATION AND THE
TENDERN TAKENTY OF THE MALTER ACTIVATION AS THE
TENDERN TAKENT OF THE MALTER ACTIVATION AS THE
THEORY OF THE MALTER ACTIVATION AS THE MALTER ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS
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                                                                                                                                                                                            remodeling; Blood
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                                                                                                                                                                                               coagulation;
                                                                                                                                                                                                                     Plasma;
PLASMIN LIGHT CHAIN B KRINGLE 1.
KRINGLE 2.
                                                             PLASMIN HEAVY CHAIN A.
ACTIVATION PEPTIDE.
PLASMIN SHORT FORM OF CHAIN
ANGIOSTATIN.
                                                                                                                                                                                            Glycoprotein; Fibrinolysis;
n; Kringle; Zymogen; Signal.
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Best Local
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01-AUG-1988
01-MAR-2002
                        MEDLINE=90076123; pubMed=2531657; Salonen E.-M., Jauhiainen M., Zardi L., V "Lipoprotein(a) binds to fibronectin and activity capable of cleaving it."; EMBO J. 8:4035-4040(1989).
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McLean J.W., Tomlison J.E., Kuang W.-J., Eato
Fless G.M., Scanu A.M., Lawn R.M.;
"CDNA sequence of human apolipoprotein(a) is
                                                                                            plasminogen.
                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                Apolipoprotein(a)
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MEDLINE=90049223;
          REVIEW
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                                                                                                                                                                                                                                                                                 RNPDGDVNGPW
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                                                                  PROTEASE ACTIVITY.
                                                                                   330:132-137(1987).
                                                                                                                                                                                                                                                                                                                         Similarity
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(Rel. 08, Last sequence update)
(Rel. 41, Last annotation update)
ein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
                                                                                                                                                                                                                                                                                                                  Conservative
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PubMed=2530631;
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90846 MW;
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REPARA E PARA E 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic acid: existence of novel and expected binding modes."; J. Mol. Biol. 256:751-761(1996).
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MEDLINE=95002201; PubMed=7918682;
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Science 246:904-910(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utermann G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytic fragmentation.
SIMILARITY: CONTAINS 38 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             naturally occuring proteolytic fragments is correlated with atherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding. MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-Ip(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: N- and O-glycosylated. The N-glycans are complex blantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, NeuNAcalpha2-3Galbeta1-3GalNAc, with smaller amounts of disialylated and non-sialylated O-glycans also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autoproteolysis. Inhibits tissue-type plasminogen activator Lp(a) may be a ligand for megalin/Gp 330.

SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin
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EMBL; X06290; CAA29618.1; PIR; S00657; S00657. HSSP; P00747; 1PMK. This InterPro; IPR001314;
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InterPro; IPR001254; or send use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement the European Bioinformatics Institute. The by non-profit institutions as long MIM; 152200; MEROPS; between SWISS-PROT entry is copyright. It is produced through an email to license@isb-sib.ch). S01.226; -. the Swiss Institute Chymotrypsin. of Bioinformatics (See http://www.isb-sib.ch/announce/ There are no rest Usage and the no restrictions by and EMBL a collaboration for in commercial 9 no

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Pfam; PF00051; kringle; 31 Pfam; PF00089; trypsin; 1 PRINTS; PR00722; CHYMOTRYI PRINTS; PR00018; KRINGLE.

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Trypsin.

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PROSITE; PS00021; KRINGLE_1; 38.

PROSITE; PS50070; KRINGLE_2; 38.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HES; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

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( PRINTS; PROUDLB; N...

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DR SMART; SMO0473; PAN_AP; 1.

DR SMART; SMO0473; PAN_AP; 1.

DR SMART; SMO0020; TRYPSC; 1.

DR PROSITE; PS00021; KRINGLE_2; 5.

DR PROSITE; PS00021; TRYPSIN_DOW; 1.

DR PROSITE; PS00134; TRYPSIN_LTS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Trypsin_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

BR PROSITE; PS00135; TRYPSIN_SER; 1.

FI SISUR remodeling; Blood coagulation; Kringle; Zymogen; Signal.

FT CHAIN 19

SIGNAL 19

STANNINGER: THEAVY CHAIN A (BY SIMILARITY PLASMIN LIGHT CHAIN B (BY SIMILARITY PLASMIN LIGHT CHAIN B (BY SIMILARITY SIGNAL B)

SERINE PROTEASE.

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Law
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
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J. Biol. Chem. 270:24004-24009(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.

LAMININ AND VON WILLEBRAND FACTOR.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00024; PAN; 1.
PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00051; kringle; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003609; Pan_app.
IPR001254; Trypsin.
0051; kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001314; Chymotrypsin.
IPR000001; Kringle.
IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1PMK
                                                                                                                                                                                                     SIMILARITY).
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Marti T., Schaller J., Rickii E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vilegenthart J.F.;
The Marting J.P., van Halbeek H., Vilegenthart J.F.;
The Martin Gerwig G.J., van Halbeek H., Vilegenthart J.F.;
The Martin Germin Germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88185329; PubMed-3356193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     miniplasminogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli "Amino acid sequence of the heavy chain of porcine plasmin. of the carbohydrate attachment sites with the human and bov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN 1988 (Rel. 06, Created)
01-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Plasminogen (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 450-790.
MEDLINE=85203907; PubMed=3846533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marti T., Schaller J., Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaller J., Marti T., Roesselet Schaller J., Marti T., Roesselet S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P06867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLMN_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibrinolysis 1:91-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
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                                                                                                          ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE. PTW: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SIALIC ACID AND IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALMAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RNPDGDVGGPW 11
MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THI
                                                                                                  (MICROHETEROGENEITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 149:279-285(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352
352
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456
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562
760
339
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KRINGLE 3.

KRINGLE 4.

KRINGLE 5.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

OHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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0.033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     porcine
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                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                           HGFL_MOUSE
                                                                                                                                                                                                                                                                                                                 Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; 1.
growth factor-like protein: expression during development.";
                                                                                                                           Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP).
MST1 OR HGFL.
                                                                                                                                                      P26928;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
        STRAIN=BALB/C; TISSUE-Liver;
MEDLINE=92002017; PubMed=1832957;
Friezner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
"Characterization of the mouse cDNA and gene coding for a
                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                          SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=10090;
                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                             HGFL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY. PIR; A25834; A25834. PIR; S03733; S03733. HSSP; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314;
InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlycoSuiteDB; P06867;
                                                                                                                                                                                                                                                                    512 RNPDGDDNGPW 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003609;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.233;
                                                                                                                                                                                                                                                                                          1 RNPDGDVGGPW 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00130; KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease; Plasma; Glycoprotein; Fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                              790 AA;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            561
561
166
256
358
461
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         560
790
790
162
243
333
333
435
602
740
289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood coagulation;
                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                             88592 MW;
                                                                                                                                                                                                                                                                                                                            81.8%;
                                                                                                                                                                                                                                                                                                                                      76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan_app
                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC...).
/FTId=CAR_000019.
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                           Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRINGLE
KRINGLE
                                                                                                                                                                                                                                                                                                                                                                        O-LINKED (GALNAC. . .).
/FTId=CAR_000020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMIN HEAVY CHAIN PLASMIN LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE.
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                            F04EA06E74BCD58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FALSE_NEG.
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                          716 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kringle; Zymogen
                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                     Length 790;
        hepatocyte
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                              0;
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PRINTS; PRO0722; ČHYMOTRYPSIN.
PRINTS; PRO0018; KRINGLE.
SMART; SM00109; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                   DISULFID
DISULFID
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 30:9781-9791(1991).
-!- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY,
CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SI
                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               DISULFID
                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                     Kringle;
                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                    D; MGI:96080; Hgfl.
tearPro; IPR001314; Chymotrypsin.
tearPro; IPR000001; Kringle.
tearPro; IPR003014; PAN.
tearPro; IPR003609; Pan_app.
tearPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 4 KRINGLE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
JUST BEFORE BIRTH THI
STABLE AFTERWARDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: MAY BE CLEAVED AFTER AA 488, HELD TOGETHER BY DISULFIDE BONDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONSERVED
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  l; kringle; 4.
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AAA50167.1;
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  HE LEVEL INCREASES DRAMATICALLY
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BY SIMILARITY.
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KRINGLE
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SERINE PROTEASE-LIKE.
BY SIMILARITY.
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THRB_BOVIN
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CONFLICT
SEQUENCE
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CARBOHYD
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MEDLINB=88245190; PubMed=3379642;
Irwin D.M., Robertson K.A., Macgillivray R.T.A.;
"Structure and evolution of the bovine prothrombin
J. Mol. Biol. 200:31-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cranial
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                  prothrombin fragment 1.";
Biochemistry 25:3977-3982(1986).
                                                                                                                                                                                                                                                                       Magnusson S., Sottrup-Jensen L., Peters
(In) Hemker H.C., Veltkamp J.J. (eds.);
Boerhaave symposium on prothrombin and
pp.25-46, Leiden University Press, Leid
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=84203525; PubMed=6326805;
McGillivray R.T.A., Davie E.W.;
                     "The Ca2+ ion and membrane binding prothrombin fragment 1."; Biochemistry 31:2554-2566(1992).
                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MEDLINE=86296631; PubMed=3741841;
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                                                       MEDLINE=92190185; PubMed=1547238; Soriano-Garcia M., Padmanabhan K.
                                                                                                                 "Structure of bovine resolution.";
                                                                                                                                         MEDLINE=91311686; PubMed=1856869;
Seshadri T.-P., Tulinsky A., Skrz
                                                                                                                                                                                                                         Park C.H., Tulinsky A.;
                                                                                                                                                                                                                                   MEDLINE=86296631;
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                                                                                                                                                                                                                                                                                                                                              Biochemistry 23:1626-1634(1984).
                                                                                                                                                                                                                                                                                                                                                                   "Characterization of bovine prothrombin mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION
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716 AA;
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                                                        Padmanabhan K.,
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                                             de Vos A.M., Tulinsky A.; structure of the Gla domain
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use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
  EMBL; V00135;
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                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edward. "The Structure of residues 7-16 of the A alpha-chain of human fibrinogen bound to bovine thrombin at 2.3-A resolution.";

The Biol Chem 267,7811.7820,11821
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                                                                     European Bioinformatics Institute.
                                                                                                                                                     FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO BY FACTOR XA.
SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KN
                                                                                                                                                                                                                     MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PREPIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITELEL HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                         CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF PROTHROMBIN TO THROMBIN.
                                                                                                                               DATABASE: NAME=ProZyme technical fact sheet;
                                                                                                                                            TRYPSIN FAMILY
                                                                                                                 WWW="http://www.prozyme.com/technical/thrombindata.html".
                                                                                                                                                                                                    MISCELLANEOUS:
                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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  CAA23451.1;
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                                                                                                                                                                                                    THROMBIN CAN ITSELF CLEAVE
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rombin gene.";
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)11; GLU_CARBOXYLATION; 1
)21; KRINGLE_1; 2.
)70; KRINGLE_2; 2.
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P14210; Q9UUG; Q9BYLG;
01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hepatocyte growth factor precursor (Scatter factor) (SF)
                                                                                                                                                                                                                                                                                                                    Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T., Asami O., Hagiya M., Nakamura T., Shimizu S.; Rasani O., Pagiya M., Nakamura T., Shimizu S.; "Isolation and expression of cDNA for different forms of hepgrowth factor from human leukocyte."; Biochem. Biophys. Res. Commun. 172:321-327(1990).
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Arakaki N., Nakayama H., Hirono S.,
Gohda E., Daikuhara Y., Kitamura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91340155; PubMed=1831432;
Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
"Organization of the human hepatocyte growth factor-encoding gene.";
                                                                                                                               TISSUB-Embryonic fibroblast;
MEDLINE-91334393; PubMed-1831266;
Weidher K. M., Arakaki N., Hartmann G.,
Rieder H., Fonatsch C., Tsubouchi H., I
                                                                                                                                                                                                                          Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M., Sugimura A., Tashiro K., Shimizu S.; "Molecular cloning and expression of human hepatocyte growth factor.";
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Mammalia; Eutheria;
                                                                                                                                                                                                    Nature
[5]
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MEDLINE=91025062; PubMed=2145836;
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                                                                                 Birchmeier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and sequence analysis of cDNA
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 SEQUENCE OF 249-695 FROM N.A.
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                                      Elliot G.,
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Primates;
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                        Angell S.; the EMBL/GenBank/DDBJ databases
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Pred. No.
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BAA14348. BAA14348. BAA14348. BAA14348. BAA14348.

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EMBL; EMBL; or send an

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BAA14348.1; BAA14348.1; BAA14348

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email to license@isb-sib.ch).

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MEDLINE=93129192; PubMed=1482348
Shimizu N., Hara H., Sogabe T.,
Nakamura T., Shimizu S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyazawa K., Kitamura A., Kitamura N.; "Structural organization and the transcription initiation site human hepatocyte growth factor gene."; Biochemistry 30:9170-9176(1991).
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                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See
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Lokker N.A., Mark
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                                                                                                                                                                                               the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98154323; PubMed=9493272;
Zhou H., Mazzulla M.J., Kaufman J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 31-127
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een the Swiss Institute of Bioinformatics and the EMBL outst
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Mark M.R., Luis E.A.,
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SMART; SM00473; PAN AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
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InterPro; IPR003014; PAN.
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1BHT; 18-NOV-98.
PF00051; kringle; 4.
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                                                 Similarity 72. 8; Conservative
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AAA52663.1; -
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                                                                 MGD; MGI:96079; Hgf.
InterPro; IPR001314;
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                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatocyte growth factor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression of the mouse Hgf/scatter factor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chin. Biophys. Acta 1216:299-303(1993).

FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOCYTOPHIC FACTOR, AND ACTS AS GROWTH FACTOR FOR A HOAD SPECTRUM OF TISSUES AND CELL TYPES. IT HAS NO DETECTABLE PROTEASE ACTIVITY.

SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
                                                                                               L; D10212; BAA01064.1;

D10213; BAA01065.1;

L; S71816; AAB31855.1;

L; X72307; CAA51054.1; A

P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 4 KRINGLE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: A SHORT FORM OF HGF IS ALTERNATIVE RNA SPLICING. THE SEQUENCE SHOWN
                                                                                                                                                                                                                                                                                                                                TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFIDE BOND.
   IPR001254;
                  IPR003609;
                                IPR003014;
                                               IPR000001;
Trypsin
                                PAN.
                                            Chymotrypsin.
Kringle.
               Pan_app.
                                                                                                                 ALT_INIT.
                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor)
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Search completed: November 8, Job time: 10.3333 secs
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Best Local S
Matches 8
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pfam; pF00024; pAN; 1.
pfam; pF00082; trypsin; 1.
pfam; pF00082; trypsin; 1.
pRINTS; pR00722; CHYMOTRYPSIN.
pRINTS; pR00718; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00020; TRYP_SPC; 1.
pROSITE; pS00070; KRINGLE_1; 4.
pROSITE; pS50270; KRINGLE_2; 4.
pROSITE; pS50270; KRINGLE_1; 4.
pROSITE; pS50270; KRINGLE_1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; Kringle; G
Signal; Alternative splic
SIGNAL 1 32
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CHAIN 496 728
MOD_RES 33 33
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                                                                                                                                           1 RNPDGDVGGPW 11
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79 RNPRGEEGGPW 189
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32
495
728
733
                                                                                                                                                                                                                                                                                                                        69.3%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                               HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
HEPATOCYTE GROWTH FACTOR BETA CHAIN.
HEPATOCYTE GROWTH FACTOR BETA CHAIN.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).

KRINGLE 1.

KRINGLE 3.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-SISING (IN SHORT ISOFORM).
N-> K (IN REF. 2).

N-> H (IN REF. 2).

N-> H (IN REF. 2).

N-> H (IN REF. 3).

R-> H (IN REF. 3).
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                                        2002,
                                                                                                                                                                                                                                                                                       Score 52; DB 1; Length 728; Pred. No. 0.61; 1; Mismatches 2; Indels
                                            09:33:52
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Gaps
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:31:21; Search time 31 Seconds (without alignments) 82.410 Million cell updates/sec

US-09-657-431-9 138

Perfect score:

Sequence: 1 RNPDGDVGGPWAYTTNPRKLYDY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

			Database :
19: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:* 20: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* 21: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* 22: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*	13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.uA1: * 14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: * 15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: * 16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: * 17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: * 18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *	6: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.bA1:* 7: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.bA1:* 8: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* 9: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1988.bA1:* 10: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.bA1:* 11: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.bAT:* 12: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.bAT:*	A_Geneseq_032802:* 1: /SIDS1/gcgdatta/geneseq/geneseqp-emb1/AA1980.DAT:* 2: /SIDS1/gcgdatta/geneseq/geneseqp-emb1/AA1981.DAT:* 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:* 5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

97.1 93 21 AAB01913 Human 97.1 95 21 AAB01913 Human 97.1 95 21 AAB01913 Human	Result SQ	· ·	Query Query Ler 	Length DB 23 2: 23 2: 24 2 79 1 79 1 20 20 20 20 20 20 20 20 20 20 20 20 20 2		ID AABS2096 AABS2096 AABS2099 AABS2099 AABS2095 AABS2095 AABS2095 AAW19256 AAW19256	
97.1 95 21 AABU1913	087554221	138 138 138 138 138 138 134 134 134 134	100.0 100.0 100.0 100.0 100.0 97.1 97.1 97.1	23 23 24 24 29 90 91	22 22 22 22 22 23 21 21	AAB92096 AAB36570 AAB92090 AAB92090 AAB92095 AAB92095 AAB92095 AAB91914 AAY58868 AAB01914 AAY58868	Laminin fragment S Mammalian kringle Laminin fragment S Laminin fragment S Mammalian kringle Human plasminogen Human plasminogen Human plasminogen

50	49	48	47	46	45	44	43	42	41	40	39	38	37	3 6	ა 5	34	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	<u>1</u> 8	17	16	15	14	13	12
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97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1	97.1				•	•	7.	7.	97.1	7.	97.1	97.1
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7	12	12	21	21	20	20	18	14	12	12	12	12	12	11	13	22	21	21	21	22	15	20	L W	13	19	13	<u>1</u> 3	20	21	22	22	22	21	21	21	21	21	18
AAR12943	AAR12939	AAR12933	AAY53867	AAY82690	AAY02114	AAY08685	AAW31169	AAR34428	AAR12938	AAR13221	AAR13220	AAR12406	AAR13219	AAR08065	AAR20013	AAG67223	AAY50867	AAY99589	AAB01887	AAB36562	AAR60519	AAY02100	AAR22503	AAR22499	AAW51457	AAR22504	AAR22502	AAY25408	AAB08407	AAU32136	AAU32129	AAU32126	AAB01919	AAB01918	AAB01915	AAB01912	AAB01890	AAW34286
	plasminogen mutein		- CC	prasil		human prasminogen	Plasminogen procei	Sequence encoded b		Human prasminogen		numan	human	prasmr	PA mutant Pig 1-54		prasi	Human plasminogen.		· i-	Human 'Giu' piasmi		[GARSYQ] - [Plasmino	[GARSYQ] - [Plasmino	Human plasminogen	[GARSYQ]-[Plasmino	[GARSYQ] - [Plasmino	Human tissue facto	A human anglogenes	Novel human secret	Novel human secret		Human plasminogen	Human kringle 5 pe				

ALIGNMENTS

AAB92096 RESULT 1 Laminin fragment SEQ ID NO:1272. AAB92096; AAB92096 standard; Peptide; 23 AA. 22-JUN-2001 (first entry)

Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.

Synthetic. Homo sapiens.

WO200069900-A2.

23-NOV-2000.

17-MAY-2000; 2000WO-US13576

17-MAY-1999; 10-SEP-1999; 15-OCT-1999; 99US-0134406. 99US-0153406. 99US-0159783.

(CONJ-) CONJUCHEM INC.

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Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a modified therapeutic peptide (I) C comprising a therapeutically active amino acid region (III) and a CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to CG a less therapeutically active amino acid region (IV), which covalently CC bonds with amino/hydroxyl/thiol groups on blood components to form a CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids. CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth CC factors and neurotransmitters, to protect them from peptidase activity CC in vivo for the treatment of various disorders. Endogenous therapeutic CC in vivo for the treatment of various disorders they require frequent CC administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or CC reduces the action of peptidases to increase length of activity (half contrace) and specificity as bonding to large molecules decreases contrace intrace and interference with phonographs of activity in the process of intrace).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                             Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis; capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                    Bridon DP, Rasamoelisolo M,
                                                                          (CONJ-) CONJUCHEM INC.
                                                                                                                17-MAY-1999;
                                                                                                                                                  17-MAY-2000; 2000WO-IB00763.
                                                                                                                                                                                             23-NOV-2000
                                                                                                                                                                                                                               WO200070665-A2
                                                                                                                                                                                                                                                                                               haemangioma; Kasposi's sarcoma; neovascularisation; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian kringle 5 peptide SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36570 standard; Peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular uptake and interference with physiological processes AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 611; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPWAYTTNPRKLYDY 23
2001-090970/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                          9905-0134406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                Thibaudeau K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 138; DB 22;
Pred. No. 4.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                              Beliveau R;
                                                                                                                                                                                                                                                                                               growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 3
AAB92090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a modified anti-angiogenic peptide (I) CC comprising a reactive group that reacts with amino groups, hydroxyl CC groups or thiol groups on blood components to form stable covalent co bonds. The reactive group is selected from succinimidyl or maleimido GC groups. (I) can have anti-inflammatory, vasotropic, cytostatic, antirheumatic, antipsoriatic, antidiabetic, antiarteriosclerotic and CC extending the in vivo half-life of a kringle 5 peptide in a patient to provide an anti-angiogenesis in a human, where the derivative is reacted CC extending the in vivo half-life of a kringle 5 peptide in a patient to peptide can be used for treating inflammatory disorders (e.g. immune and CC experience associated with inappropriate or inopportune invasion of CC capillary proliferation in atherosclerotic plaques or osteoporosis, or metastases, angiofibromas, retrolental fibroplasia, haemangiomas, cCC casposi's sarcoma or other cancers requiring neovascular sation to support tumour growth). The peptides are useful for treating these CC diseases in mammalian or human pattents. AAB36567 represents a mammalian CC claimed kringle 5 peptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                          17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                           (CONJ-) CONJUCHEM INC
                                                                                                                                        17-MAY-2000; 2000WO-US13576
                                                                                                                                                                        23-NOV-2000
                                                                                                                                                                                                       WO200069900-A2
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                       Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               AAB92090;
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB92090 standard; Peptide; 24 AA.
                                                                                                                                                                                                                                                                            nydroxyl; thiol; hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                            Laminin fragment SEQ ID NO:1266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 9; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                        99US-0134406.
99US-0153406.
                                                                         9908-0159783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 4.4e-11;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0,

Bridon DP,

Ezrin AM,

Milner PG,

Holmes DL,

Thibaudeau K;

WPI; 2001-112059/12

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RESULT 4
AAB92015
ID AAB8
XX AAB
AC AAB8
XX Cambridge
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB92095 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 609;
                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxyl; thiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laminin fragment SEQ ID NO:1271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                             Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000
                                                                                                                             WPI; 2001-112059/12
                                                                                                                                                                                                                                                 (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                       DP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                    Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽,
                                                                                                                                                                                                                                                                                                                                            99US-0134406
99US-0153406
                                                                                                                                                                                                                                                                                                               99US-0159783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hormone; growth factor; neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         733pp; English
                                                                                                                                                                                       Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 138; DB 22;
Pred. No. 4.6e-11;
; Mismatches 0;
                                                                                                                                                                                       Holmes DL,
                                                                                                                                                                                           Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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RESULT 5
AAB36565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a creative group (II) (e.g. succinimidy) and maleimido groups) attached to reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular uptake and interference with physiological processes AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasotropic; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism; psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 611; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalian kringle 5 peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                             New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                      17-MAY-2000; 2000WO-IB00763
                                                                                                                                                                                                                                                                                                                                          WO200070665-A2
                                                                                                                                                                                                                                                                                                                                                                              Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                   capillary proliferation; atherosclerotic plaque; osteoporosis;
cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
                                                                                                                                                           Bridon DP,
                                                                                                                                                                                                                                  17-MAY-1999;
                                                                                                                                                                                                                                                                                                          23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                haemangioma;
                                                                                                                                                                                             (CONJ-) CONJUCHEM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPWAYTTNPRKLYDY 23
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                                                                                                                          2001-090970/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                           Rasamoelisolo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Kasposi's sarcoma; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀΑ;
                                                                                                                                                                                                                                  99US-0134406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 138; DB 22;
Pred. No. 4.6e-11;
); Mismatches 0;
                                                                                                                                                              Thibaudeau K,
                                                                                                                                                              Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                    tumour growth.
                                                                                                                                                                Beliveau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                <del>بر</del>
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Claim 5; Page 9; 82pp; English

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AAW19256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
         corresponding
                                        This sequence
                                                                                                                                                Plasminogen Kringle 5 peptide - which inhibits endothelial cell proliferation, useful to treat angiogenesis mediated diseases and detection and diagnosis
                                                                                              Claim 1; Page 8; 51pp; English.
                                                                                                                                                                                                                                                                                    WPI; 1997-350965/32.
                                                                                                                                                                                                                                                                                                                                                Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen; Kringle 5; diagnosis; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1996;
13-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human plasminogen Kringle 5 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW19256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW19256 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a modified anti-angiogenic peptide (I) comprising a reactive group that reacts with amino groups, hydroxyl groups on thiol groups on blood components to form stable covalent bonds. The reactive group is selected from succinimidyl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claimed kringle 5 peptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                Folkman MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kringle 5; cell proliferation inhibitor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                     S.
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95US-0008519.
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   an isolated fragment of the amino acid 462 of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 138; DB 22; Pred. No. 4.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
Kringle 5 pe
plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                               peptide
protein which
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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours

Example 17; Page -; 48pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                              WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                         03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corneal diseases, rubeosis, neovascular glaucoma, diabetic retinopathy, retrolental fibroplasia, arthritis, diabetic neovascularisation, muscular degeneration, peptic ulcer, Helicobacter related disease, fractures, keloids, vasculogenesis, haematopoiesis, ovulation, menstruation, placentation or cat scratch fever, and to stimulate wound healing. The protein and antibodies generated from it can be used to
                                                                                                                                                                    incubation and isolation
                                                                                                                                                                            unsorders such as angiogenic, ocular, involves mixing mammalian plasminogen
                                                                                                                                                                                                 disorders such as angiogenic,
                                                                                                                                                                                                           Preparation of Kringle five peptide fragment for treating various
                                                                                                                                                                                                                                                                            Davidson DJ;
                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               US6057122-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiangiogenic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human plasminogen kringle 5 (Val454-Ala543).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB01914 standard; Protein; 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used in a novel method to inhibit endothelial cell proliferation activity. The protein can be used to treat angiogenesis mediated diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis, telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial angiogenesis, plaque neovascularisation, coronary or cerebral collaterals, arteriorenous malformations, ischemic limb angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       healing. The protein and antipoutes years. In detection, imaging and screen for agonists and antagonists or in detection, imaging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 RNPDGDVGGPWCYTTNPRKLYDY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                       96US-0643219
                                                                                                                                                                                                                                                                                                                                         97US-0832087
                                                                                                                                                                                                                                                                                                                                                                                    97US-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134; DB 18;
Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                               skin diseases and cancer, and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RRESULT 8
AAXYSMEN ID
AAXYSMEN ID
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DT 16-Y

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratce disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta sequences AAB01906-B01919 represent fragments of human plasminogen us in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-angiogenic; angiogenesis inhibitor; cancer; tumour; therapy;
plasminogen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2000
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                                                                                                                                                               of anti-angiogenic polypeptides. (I) comprise 2 or more heterologous membrane binding elements (MBEs, see AAY58855-61) with low membrane affinity that are covalently attached to a soluble anti-angiogenic polypeptide such as a non-catalytic region of human plasminogen. The MBEs interact independently with thermodynamic
                                                                                                                                                                                                                                                                                                                          The present sequence is that of human plasminogen mature polypeptide. The invention relates to new soluble derivatives (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New soluble derivative of anti-angiogenic polypeptide useful for treatment of primary or secondary cancers, contains covalently attached membrane-binding elements for targeting .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200004052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human plasminogen mature polypeptide.
                                                              additivity, with components of the vascular endothelium. (I) provide targeted delivery of the anti-angiogenic polypeptide to cell membranes and sites of active angiogenesis, particularly the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith RAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 21; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADPR-) ADPROTECH PLC
concentration and reduce the risk of adverse effects on normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 RNPDGDVGGPWCYTTNPRKLYDY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is not shown in the specification, but is derived the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bright JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0015505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-GB02292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.1%;
95.7%;
                                         and therefore increase the local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steward M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 5.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasminogen used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cat scratch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                      The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             processes elsewhere in the vasculature. They are umethod of treatment of primary or secondary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human plasminogen kringle 5 (Val454-Phe546).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB01917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01917 standard; Protein;
                                                     Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta.
                                                                                                                                                   lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000
Sequences AAB01906-B01919 represent fragments in an exemplification of the invention.

Note: This sequence is not shown in the specif
                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPDGDVGGPWCYTTNPRKLYDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Similarity
22; Conser
   sequence is not shown in the specification, but is derived
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134; DB 21;
Pred. No. 5.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       They are used in a claimed
                                             of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 91;
                                             plasminogen used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                  The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber Stronger of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber osceritation of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber osceritation of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber osceritation of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber osceritation of the prophylaxis of various autoimmune diseases (e.g., haemangiomas, osler-Webber osceritation of the prophylax
                                         endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratt disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen w
                               Sequences AAB01906-B01919 represent frain an exemplification of the invention
                                                                                                                                                                     Syndrome), diseases caused by excessive or abnormal stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davidson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 17; Page -; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involves mixing mammalian plasminogen and elastase incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-349573/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human plasminogen kringle 5 (Val449-Ala543).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB01913 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; kringle domain; endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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is not shown in the specification, but is derived
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95.7%;
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                                            human plasminogen used
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                                                                                                                            cat scratch
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CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and Cc endothelial cell proliferation and migration. The peptides are useful CC for treating angiogenic diseases, primary and metastatic solid tumours CC and carcinomas of various organs such as breast, genital tract, CC endocrine glands, skin, tumours of the brain and eyes and solid tumours CC arising from haematopoietic malignancies such as leukaemias and CC lymphomas. They are also used for the prophylaxis of various autoimmune CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber CC syndrome), diseases caused by excessive or abnormal stimulation of CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases CC which have angiogenesis as a pathologic consequence (e.g., cat scratch CC disease and ulcers). The peptides are also useful as a birth control CC agent which inhibits ovulation and establishment of the placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
AAB01916
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Best Local
       Sequences AABO1906-B01919 represent fragments in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                             The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammallan plasminogen and
                                                                                                                                                                                                                                                                                                peptide fragments. The method comprises mixing elastase in the ratio 1:100-1:300, followed by
                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                     Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipporiatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 RNPDGDVGGPWCYTTNPRKLYDY 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the full length human plasminogen sequence (AAB01887) shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97us-0832087.
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 5
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.8e-10;
                                                                                                                                                                                                                                                                                                  incubating and isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 95
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Note: This sequence is not shown

in the specification, but is derived

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ARMS44286
ID AAMS4
XX AAMS4
XX 14-MA
XX 14-MA
XX 14-MA
XX Plasm
KW Plasm
KW Plasm
KW autoj
XX WO974
XX AABB
PR 03-MA
XX WAPI;
XX New ;
PT Plasm
CC C Plass
CC Plass
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CC Anti
CC Lymp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer; metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma; psoriasis; arthritis; macular degeneration; diabetic retinopathy; autoimme disease; ocular disease; capillary proliferation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           figure
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                       joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)sogonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kringle 5 receptor.
                                                                                                                                                                                                                                                                                                                                                                                     fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophiliac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 35; Fig 2; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-558670/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davidson DJ, Gubbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, psoriasis, arthritis etc., including gene therapy
normal cells. Typically they have 800-times greater inhibitory activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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96US-0643219
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Pred. No. 6e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber (e.g., haemangiomas, osler-Webber)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen; kringle 5 domain; endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2000
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03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human plasminogen kringle 5, SEQ ID NO:34.
                                          syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01890-B01894 represent, respectively, human, murine, Rhesu monkey, bovine and porcine plasminogen kringle 5 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davidson DJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of preparing plasminogen kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 RNPDGDVGGPWCYTTNPRKLYDY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
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97US-0832087.
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95.78;
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                                                                                   human, murine, Rhesus
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Sequence

101 AA

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                                                                         (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of anglogenesis and endothelial cell proliferation and migration. The peptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from because the control of the brain and eyes and solid tumours arising from because the control of the brain and eyes and solid tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-349573/30.
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03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2000
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97US-0832087.
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95.7%;
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Pred. No. 6.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eyes and solid tumours
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Sequence

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RESULT 15
AAB01915
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                                                                                                                                                                                                                                       endothelial cell proliferation and migration. The peptides are useful for treating anglogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber Syndrome), diseases caused by operations (e.g., haemangiomas, Osler-Webber Syndrome), diseases caused by operations
                                                                                                             which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating
                                                                                                                                                                                           Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), disease
                                                                                                                                                                                                                                                                                                                                                                                         the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                    in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6057122-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human plasminogen kringle 5 (Val443-Phe546).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB01915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB01915 standard; Protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 RNPDGDVGGPWCYTTNPRKLYDY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                  s sequence is not shown in the specification, but is derived full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134; DB 21;
Pred. No. 6.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                    diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 16
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                    The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoletic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber (e.g., haemangiomas), osler-Weber (e.g., haemangiomas), osler-Weber (e.g., haemangiomas), osler-Weber (e.g., haemangiomas), osler-Weber (e.g., haem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasminogen; human; kringle domain; endothelial cell proliferation;
angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
antipporiatic; antiinflammatory; antialcer; antiheumatic; antiarthritic;
antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01918 standard;
                                                                                                                              Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human plasminogen kringles 4-5 (Val355-Ala543).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-349573/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBO ) ABBOTT
                                                      figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 RNPDGDVGGPWCYTTNPRKLYDY 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                full length human plasminogen
                                                                                                       sequence is not shown in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0643219.
97US-0832087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 6.4e-10;
                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 104;
                                                                                   (AAB01887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                but is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Sequence

Sequence

192 AA

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RESULT 17
AAB01919
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                                                                endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoletic malignancles such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, osler Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; human; kringle domain; endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB01919 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                     peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human plasminogen kringles 4-5 (Val355-Phe546).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of preparing plasminogen kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 RNPDGDVGGPWCYTTNPRKLYDY
                                    figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY
                                                   This sequence is not shown in the specification, but is derible the full length human plasminogen sequence (AAB01887) shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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97US-0832087.
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95.7%;
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Pred. No. 1.2e-09;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for the polypeptides are useful for the determining the presence of or predisposition to a disease associated to with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells to the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or the nucleic acids encoding the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically cengineered to express them are also useful for producing the proteins. They may be used to therapy, and can be used as nutritional supplements. They may be used to concrease stem cell proliferation; to regulate haematopoiesis; and in treatment of leukaemias. ANU29510-ANU33304 represent the amino acid cequences of novel human secreted proteins of the invention.
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                                                                  Matches
                                                                                              Query Match
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Best Local :
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 558; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU32126 standard; Protein; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted protein #2617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
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                                                                                Local
                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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RNPDGDVGGPWCYTTNPRKLYDY 131
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                           266 AA;
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                            97.18;
95.78;
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95.7%;
                                                             0;
                                                                          Score 134; DB 22; Pred. No. 1.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 134; DB 21; Length 192; Pred. No. 1.2e-09;
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                       Length 266;
                                                           Indels
                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                         0,
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RESULT 20
AAU32136
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AAU32129
                                                                                                                                                                                                Matches
AAU32136
                                                                                                                                                                                                                                                                                                          for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used tincrease stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent
                                 AAU32136 standard; Protein; 266 AA
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                 sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 559; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopolesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                                                                                                          109 RNPDGDVGGPWCYTTNPRKLYDY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-2001; 2001WO-US08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU32129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU32129 standard; Protein; 266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                           1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                 Local
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Drmanac
                                                                                                                                                                                                                                                                   266 AA;
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                            97.1%;
95.7%;
                                                                                                                                                                                             0;
                                                                                                                                                                                         Score 134; DB 22;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                            Length 266;
                                                                                                                                                                                           0;
                                                                                                                                                                                           Gaps
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18-DEC-2001

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RESULT 21
AAB08407
ID AAB08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated cwith altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells can be compared to the proteins are useful for identifying a therapeutic agent compressing the proteins are useful for identifying a therapeutic agent compression or physiological interactions of the polypeptide. Vectors comprising compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to express them are also useful for producing the proteins. Compineered to expression and/or nearesticing to regulate haematopoiesis; and in the cartilage, tendon and/or stimulation; as anti-inflammatory agents; and compineered to the compineered to the proteins. Compineered to the proteins and compineered to the proteins of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding a range of human vaccination, testing and therapy - \ensuremath{\mathbf{T}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179449-A2
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                                 Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease;
                                                                                                                                                                             A human angiogenesis inhibitor designated KED
                                                                                                                                                                                                                                                                                                                                                                                                   AAB08407 standard; Protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2001; 2001WO-US08656.
adult respiratory distress syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 RNPDGDVGGPWCYTTNPRKLYDY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to novel human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n; vaccination; gene therapy; nutritional supplement;
cell proliferation; haematopoiesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 561; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 134; DB 22;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
Castleman's disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic
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RESULT 2:
AAYZ5408
ID AAYY
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AC AAYY
XX
DT 08-9
DT 08-9
DT 15:
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Vass

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1999;
25-FEB-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human polypeptide which is a potent angiogenesis inhibitor, designated KED. The KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome, castleman's disease, psoriasis, hepatitis, aneurysm, renal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY25408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FORD-) FORD HEALTH SYSTEM HENRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2000;
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                                                                                                                                                                 01-JUL-1999
                                                                                                                                                                                                                        WO9932143-A1
                                                                                                                                                                                                                                                                                                                                                             Tissue factor; human; thrombogenic; substructure; thrombose; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human tissue factor clone NuV129 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY25408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and haemangioma.
(NUVA-) NUVAS
                                                      23-DEC-1997;
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                vasculative malformation; vascular endothelium; NuV129
                                                                                                          22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNPDGDVGGPWCYTTNPRKLYDY 78
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AA;
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99US-0121633.
99US-0166176.
                                                                                                             98WO-US27498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 134; DB 21;
Pred. No. 1.6e-09;
0; Mismatches 1;
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RESULT 23
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XX EJASM
CW AAR22
XX PLASM
XX PLASM
XX PLASM
XX PLOOD
ET Regio
FT Regio
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FT Cleav
FT Cleav
FT Cleav
YX W0920
XX W0920
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                    Dodd I,
                                                                (BEEC ) BEECHAM GROUP PLC
                                                                                                               01-SEP-1990;
                                                                                                                                                      29-AUG-1991;
                                                                                                                                                                                                    19-MAR-1992
                                                                                                                                                                                                                                                WO9204450-A
                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen; tissue plasminogen activator; hybrid; fibrinolysis; blood clotting; acute myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              where the entity imparts thrombogenic activity when positioned in the function-forming-context at the biologically susceptible sites, and the entity has no thrombogenic activity absent a function-forming-context at the biologically susceptible sites. The context-dependent functional entities impart thrombogenic activity only at biologically susceptible sites. They can be used to obliterate vasculative malformations or to selectively thrombose the vasculature of solid tumours. This sequence represents the human tissue factor protein NuV129 which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel thrombogenic polypeptides which comprise a thrombogenic substructure and a context-dependent entity which recognizes desired biologically susceptible sites, e.g. tumour vascular endothelium.
                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR22502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR22502 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickinson CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [GARSYQ]-[Plasminogen 443-541]-[t-PA 262-527] hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombogenic potential and one or more context-enhancing substructures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel context-dependent functional entity comprises a substructure with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New thrombogenic polypeptides used to,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX78893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPDGDVGGPWCYTTNPRKLYDY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-405116/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the ability to recognize desired biologically susceptible sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                  Brown M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 85-88; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                          90GB-0019120
                                                                                                                                                      91WO-GB01455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                                                                                                                                                              /note=
119..1
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "amino acids -3 to +3 of t-PA"
7...105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        106..371
                                                                                                                                                                                                                                                                                                                                                                             /note=
                    Robinson JH;
                                                                                                                                                                                                                                                                                                                 .120
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95.7%;
                                                                                                                                                                                                                                                                                     "t-PA cleavage site"
                                                                                                                                                                                                                                                                                                                                                                        "amino acids 443-541 of plasminogen"
                                                                                                                                                                                                                                                                                                                               "amino acids 262-527 of t-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. obliterate vasculative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
2.2e-09;
nes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
This hybrid plasminogen/u-PA sequence is described in the specification although the sequence itself is not given.
                                                                 Hybrid plasminogen activators for treating thrombotic disease comprise Kringle 5 or Kringles 4 and 5 of plasminogen linked B-chain of t-PA or u-PA via aminoacid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This hybrid plasminogen/t-PA sequence is described in the specification although the sequence itself is not given. The sequence given here has been compiled using the human plasminogen sequence from Patent No. WO9013640 and the t-PA sequence of DE3930099. The variant 4-anisoyl [SYQ]-[plasminogen 443-541]-[t-PA 262-527] is also specifically claimed. The hybrid fibrinolytic enzymes are useful in the treatment of thrombotic diseases. See also AAR22499 and AAR22503-4.
                                         Claim 11; Page 50; 64pp; English
                                                                                                                           WPI; 1992-114357/14.
                                                                                                                                                     Dodd I,
                                                                                                                                                                                                           01-SEP-1990;
                                                                                                                                                                                                                                                                19-MAR-1992.
                                                                                                                                                                                                                                                                                           WO9204450-A.
                                                                                                                                                                                                                                                                                                                                  Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                     29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR22504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybrid plasminogen activators for treating thrombotic diseases comprise Kringle 5 or Kringles 4 and 5 of plasminogen linked to B-chain of t-PA or u-PA via aminoacid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR22504 standard; Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 50; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [GARSYQ]-[Plasminogen 443-541]-[u-PA 137-411] hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-114357/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNPDGDVGGPWCYTTNPRKLYDY
                                                                                                                                                                                BEECHAM GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                     Brown M, Robinson JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      urokinase-like plasminogen activator; hybrid;
; blood clotting; acute myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                           90GB-0019120
                                                                                                                                                                                                                                     91WO-GB01455
                                                                                                                                                                                                                                                                                                                                    126.
                                                                                                                                                                                                                                                                                                                                                            /note= "amino acids 443-541 of plasminogen"
106..380
                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "amino acids -3 to +3 of t-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                               "amino acids 137-411 of u-PA"
                                                                                                                                                                                                                                                                                                                    "u-PA cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence given here has been compiled using the human plasminogen sequence from Patent No. W09013640 and the human u-PA sequence from the SWISSPROT database (URCKSHUMAN). The hybrid fibrinolytic enzymes are useful in the treatment of thrombotic diseases. See also R22499, R22502 and R22503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW51457 standard; protein; 437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elastase; Sepharose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human plasminogen fragment with neovascularisation inhibiting activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                            28-NOV-1996;
                                                                                                                                                                                                                                                                                    16-JUN-1998.
                                                                                                                                                                                                                                                                                                                                  JP10158300-A.
                                                                                               WPI; 1998-393476/34.
                                                                                                                                                                                                                                     28-NOV-1996;
                        inhibiting activity
                                                Human plasminogen derived polypeptide - has neovascularisation
                                                                                                                                        (SUZM ) SUZUKI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPDGDVGGPWCYTTNPRKLYDY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                            96JP-0317250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Disulphide_bond
53..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Disulphide_bond 25..64
                                                                                                                                                                                                                                                                                                                                                                                                      383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194..313
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                                                                                                                                                                                                                                                                                                                                                                                                                          label=
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95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 13; Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form 1 and form 2; (b) separating plasminogen form 1 and form 2 and digesting them with elastase; (c) fractionating the elastase decomposed product of form 1 plasminogen and form 2 plasminogen in a lysine sepharose column; (d) collecting the fractions bound to the lysine sepharose column; (e) further fractionating the form 2 plasminogen using an Aminohexal Sepharose column; and (f) collecting the fraction bound to the Aminohexal Sepharose column. This human plasminogen fragment can be used to inhibit growth of vascular endothelial cells. The present sequence represents amino acids 355-791 of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a neovascularisation inhibitor which comprises amino acids 355-791 of human plasminogen. Also claimed are a method for the preparation of angiostatin, and angiostatin prepared by this method. The human plasminogen protein fragment is prepared by: (a) applying human the human plasminogen protein fragment is prepared by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasminogen to a lysine Sepharose column to separate it into plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR22499;
                                                                               Hybrid plasminogen activators for treating thrombotic disease comprise Kringle 5 or Kringles 4 and 5 of plasminogen linked B-chain of t-PA or u-PA via aminoacid sequence
                                                                                                                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     blood clotting; acute myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen; tissue plasminogen activator; hybrid; fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [GARSYQ]-{Plasminogen 347-541]-[t-PA 262-527] hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR22499 standard; protein;
specification although the sequence itself is not given. The
                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                    This hybrid plasminogen/t-PA sequence is described in the
                                                  Claim 8; Page 50; 64pp; English.
                                                                                                                                                                                                                                                 01-SEP-1990;
                                                                                                                                                                                                                                                                                                            19-MAR-1992
                                                                                                                                                                                                                                                                                                                                            WO9204450-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 RNPDGDVGGPWCYTTNPRKLYDY 181
                                                                                                                                                  WPI; 1992-114357/14.
                                                                                                                                                                                 Dodd I,
                                                                                                                                                                                                                                                                               29-AUG-1991;
                                                                                                                                                                                                               (BEEC ) BEECHAM GROUP PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                 Brown M, Robinson JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                 90GB-0019120
                                                                                                                                                                                                                                                                                 91WO-GB01455
                                                                                                                                                                                                                                                                                                                                                                                           /note= "amino acids 262-527 of t-PA" 215..216
                                                                                                                                                                                                                                                                                                                                                                            /note= "t-PA cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "amino acids 347-541 of plasminogen"
202..467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "amino acids -3 to +3 of t-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 19;
Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                                                                                                         diseases
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RESULT 27
AAR22503
ID AAR22
XX AAR22
XX AAR22
XX AAR22
XX 25-AU
XX Plasm
KW Plasm
KW Plasm
KW Fibri
XX Regic
FT Regic
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    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                 Sequence
                                                                                        sequence given here has been compiled using the human plasminogen sequence from Patent No. WO9013640 and the human u-PA sequence from the SWISSPROT database (UROKSHUMAN). The hybrid fibrinolytic enzymes are useful in the treatment of thrombotic diseases.
                                                                                                                                                                                                                           Hybrid plasminogen activators for treating thrombotic diseases comprise Kringle 5 or Kringles 4 and 5 of plasminogen linked to B-chain of t-PA or u-PA via aminoacid sequence
                                                                             See also R22499, R22502 and R22504.
                                                                                                                                                This hybrid plasminogen/u-PA sequence is described in the specification although the sequence itself is not given. The
                                                                                                                                                                                                  Claim 10; Page 50; 64pp; English
                                                                                                                                                                                                                                                                                                WPI; 1992-114357/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                            (BEEC ) BEECHAM GROUP PLC
                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen; urokinase-like plasminogen activator; hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [GARSYQ]-[Plasminogen 347-541]-[u-PA 137-411] hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence given here has been compiled using the human plasminogen sequence from Patent No. W09013640 and the t-PA sequence of DE3930099 A N. P.Dimethyl -4-aminobenzoyl two-chain [SYQ]-[plasminogen 347-541]-[t-PA 262-527] and the 4-anisoyl version of this variant are also specifically claimed. The hybrid fibrinolytic enzymes are useful in the treatment of thrombotic diseases. See also AAR22502-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR22503 standard; Protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 RNPDGDVGGPWCYTTNPRKLYDY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                               Brown M,
                                                 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blood clotting; acute myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                          90GB-0019120
                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-GB01455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202..476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amino acids 347-541 of plasminogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acids -3 to +3 of t-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amino acids 137-411 of u-PA"
                                                                                                                                                                                                                                                                                                                             Robinson JH;
   97.18;
95.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.18;
95.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "u-PA cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
Score 134; DB 13; Pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134; DB 13;
Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Вb Q

532

1 RNPDGDVGGPWAYTTNPRKLYDY 23

Matches Query Match

22;

Conservative

0;

Mismatches

Local

Similarity

97.1%; 95.7%;

Score 134; DB 20; Pred. No. 3.4e-09;

Length 566; Indels

0;

Gaps

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AAY02100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                       anti-anglogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes multifunctional proteins which comprise
                                                                                                                                                                                                                                                                                                                                                                              combinations of angiostatin, endostatin, interferon, thrombos interferon inducible protein and platelet factor m{4}, and have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 95-96; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic mediated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-255098/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolanowski MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09916889-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SEAR ) SEARLE & CO G D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor cell production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY02100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY02100 standard; Protein; 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPWCYTTNPRKLYDY 195
                                                                     The present sequence represents a multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McKearn JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0060609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casperson GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregory SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>!</del>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                           thrombospondin,
                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                        of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 30
AAB36562
IID AABB
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AC AABB
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DT Wamm
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KW Krin
KW Krin
KW Vasc
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AAR60519
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1993;
05-FEB-1993;
03-DEC-1993;
           Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory; vasotroplc; cytostatic; antirheumatic; antipsoriatic; antidiabetic; antidatetic; cateopathic; angiogenesis inhibitor; angiogenesis; inflammatory disorder; inflammation; chronic articular rheumatism;
                                                                                                       09-MAR-2001
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding kringle domains 1 and 4 of human plasminogen (full sequence given in AAR60519) was PCR amplified using primers given in AAQ71268-71. Amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage site (given in AAR60503), subcloned in vector pLCIIMLCH6 so that it was linked to a hexahistidine-encoding sequence and expressed in E. coli QX13. The fusion protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 148-50; 202pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DENZ-) DENZYME APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase chain reaction; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 'Glu' plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR60519 standard;
                                                                                                                                  AAB36562;
                                                                                                                                                            AAB36562 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9418227-A
                                                                                                                                                                                                                                                                                                                                                                          purified on an Ni2+-activated NTA-agarose column.
 psoriasis; diabetic retinopathy;
                                                                             Mammalian kringle 5 protein
                                                                                                                                                                                                                                                                                                                                                               procedure
                                                                                                                                                                                                                             512
                                                                                                                                                                                      30
                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1994-279681/34.
                                                                                                                                                                                                                             RNPDGDVGGPWCYTTNPRKLYDY 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease; Factor-Xa; recognition site; plasminogen; kringle;
protein cleavage; protein folding; primer;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                               was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              folded
                                                                                                                                                                                                                                                                                                                                     790 AA;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holtet TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93DK-0000130.
93DK-0000139.
93WO-GB02492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-DK00054
                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                           to obtain correctly folded recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                       entry)
                                                                                                                                                                                                                                                                                           97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thogersen
                                                                                                                                                            790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790
                                                                            SEQ ID NO:1.
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                               Score 134; DB 15;
Pred. No. 4.8e-09;
0; Mismatches 1;
                                                                                                                                                            ₹
neovascular glaucoma;
                                                                                                                                                                                                                                                                                                        Length 790;
                                                                                                                                                                                                                                                                                                                                                                            A cyclic
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                               AAB01887
                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a modified anti-angiogenic peptide (I) CC comprising a reactive group that reacts with amino groups, hydroxyl CC groups or thiol groups on blood components to form stable covalent CC bonds. The reactive group is selected from succinimidyl or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, CC antirheumatic, antipsoriatic, antidabetic, antiarteriosclerotic and CC extendating angiogenesis in a human, where the derivative is reacted CC for treating angiogenesis in a human, where the derivative is reacted CC with blood proteins. (I) are also useful for manufacturing a medicament CC extending the in vivo half-life of a kringle 5 peptide in a patient to CC provide an anti-angiogenic effect. In particular, a modified kringle 5 copide can be used for treating inflammatory disorders (e.g. immune and con immune inflammation, chronic articular rheumatism or psoriasis), CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis, constitution of the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     capillary proliferation in atherosclerotic plaques or osteoporosis), or cancer associated disorders (e.g. solid tumours, solid tumours, metastases, angiofibromas, retrolental fibroplasia, haemangiomas, Kasposi's sarcoma or other cancers requiring neovascularisation to support tumour growth). The peptides are useful for treating these diseases in mammalian or human patients, AAB36562 represents a mammalian or human patients, AAB36567 represents secifically kringle 5 protein, and AAB36563 to AAB36577 represent specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified anti-angiogenic kringle 5 peptides capable of forming conjugates with blood proteins, useful for treating angiogenesis, inappropriate invasion of vessels or cancers in humans or mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2000; 2000WO-IB00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capillary proliferation; atherosclerotic plaque; osteoporosis; cancer; solid tumour; angiofibroma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-090970/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200070665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia
                                                                                                                                                                                   AAB01887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claimed kringle 5 peptides from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth
                                                                                                                                                                                                                                 AAB01887 standard; Protein; 791 AA
                                                                                                                                                                                                                                                                                                                                                                      512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                 1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPWCYTTNPRKLYDY 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 74-77; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasamoelisolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĭ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 134;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beliveau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Plasminogen; human; kringle 5 domain; endothelial cell proliferation;

Human plasminogen,

SEQ ID NO:1.

18-SEP-2000

(first entry)

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RESULT 32
AAY99589
ID AAY99
XX
AC AAY99
XX
DT 13-SE
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                                                                                                                                                                                                                                      The invention relates to a method of preparing plasminogen kringle 5 CC peptide fragments. The method comprises mixing mammalian plasminogen and CC elastase in the ratio 1:100-1:300, followed by incubating and isolating CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and CC endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and CC carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising CC from haematopoietic malignancies such as leukaemias and lymphomas. They CC are also used for the prophylaxis of various autoimmune diseases (e.g., bearing CC from haematopoietic malignancies such as leukaemias and lymphomas. They CC are also used for the prophylaxis of various autoimmune diseases (e.g., bearing), CC diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atheroscienosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and conhibits ovulation and establishment of the placenta. The present
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
Disulfide-bond
              13-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                     AAY99589;
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1996;
03-APR-1997;
                                                          AAY99589 standard;
                                                                                                                                                                                                                                sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Fig 1; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davidson DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6057122-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                  513
                                                                                                                                                                            Local
                                                                                                                                      1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                 RNPDGDVGGPWCYTTNPRKLYDY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-349573/30
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA52284
                                                                                                                                                                                                            791 AA;
                                                                                                                                                              Conservative
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
462..541
483..524
512..536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0643219
97US-0832087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97us-0851350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by GTC"
                                                          protein;
                                                                                                                                                                                                                                human plasminogen.
                                                                                                                                                                        97.18;
95.78;
                                                          791
                                                                                                                                                              0;
                                                                                                                                                            Score 134; DB 21;
Pred. No. 4.8e-09;
0; Mismatches 1;
                                                          ΑA
                                                                                                                                                                                 Length 791;
                                                                                                                                                              0;
                                                                                                                                                             Gaps
                                                                                                                                                             0;
                                                                  RESULT 33
AAY50867
ID AAY50
                                                                                                                                                                                                                     EXTXXX
                                                                                                                            В
                                                                                                                                                                        Matches
Human plasminogen protein fragment.
                      24-FEB-2000 (first entry)
                                             AAY50867;
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protease zymogen in the extracellular fluids of vertebrates. Its calculated the proteolysis ascive form, plasmin, is implicated in pericellular proteolysis cassociated with a wide range of physiological and pathological corporesses. Plasminogen expression is regulated by plasminogen activators which hydrolyse a peptide bond in plasminogen to convert it to plasmin corporate to referre the plasmin. Review of sequence homologies of several convert it to plasmin. Review of sequence homologies of several plasminogen activators and chymotrypsin has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human plasminogen. Novel plasminogen activators have been made cased upon the plasminogen Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
   AAY50867 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; serine protease zymogen; cardiant; thrombolytic;
plasminogen activator; heart attack; stroke; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is plasminogen, the principal serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6,7,8; Page 20-23; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OKLA-) OKLAHOMA MEDICAL RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                               513 RNPDGDVGGPWCYTTNPRKLYDY 535
                                                                                                                                                                                                                           1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                          . Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     791 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0110588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US09991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542..791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, (claim 7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "specifically claimed in claims 7 and 8 of the
specification, preferably amino acids 562..791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "specifically
protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang JJN
                                                                                                                                                                                                                                                                                                                    97.1%;
95.7%;
   791 AA
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                    Score 134; DB 21;
Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claimed in
                                                                                                                                                                                                                                                                                                                                                         DB 21;
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                                                                                                                                                                                                                                                                                                                                                     Length 791;
                                                                                                                                                                                                                                                                                             Indels
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RESULT 34
AAG67223
ID AAG67
XX AAG67
XX AMINC
DT 13-NC
XX AMINC
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptokinase where at least one nonessential portion has been modified. The invention also describes a method of forming a thrombolytic agent comprising determining a nonessential portion to render the resulting protein less antigenic. The modified streptokinase is used to treat blood clot disorders, such as heart attacks. The modified streptokinase has less antigenicity than streptokinase but is still able to complex plasminogen and lead to plasminogen activation. Modified streptokinase with the monessential portions removed or truncated simplify the molecule. Such smaller proteins are cheaper and easier to produce. This sequence represents a fragment of the human plasminogen protein which is used in the description of the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen; human; thrombolytic agent; streptokinase; antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-052966/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     blood clot; heart attack; treatment.
                                                                                                                                                                                                                                             Angiostatin; plasminogen; sulfydryl donor; angiogenesis; tumour; angiogenic disease; neoplastic disease; connective tissue disorder; rheumatoid arthritis; atherosclerosis; ocular angiogenic disease; diabetic retinopathy; corneal graft rejection; cardiovascular disease; cerebral vascular disease; diabetes; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel thrombolytic agent comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 40-43; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New thrombolytic agents derived from modified humanized, streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG67223 standard; Protein; 791 AA
                                                                                               WO200158921-A2
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                   chronic inflammation; autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 RNPDGDVGGPWCYTTNPRKLYDY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating blood clot disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  791 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0084392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US10086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 134; DB 21;
Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 35
AAR20013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               donor, or culturing cells capable of producing plasminogen activator in conditioned culture medium (CCM) and contacting the CCM with plasminogen. Angiostatin produced by method of the invention is useful for treating animals with angiogenesis diseases. It is useful for treating an angiogenic disease such as neoplastic diseases (e.g. tumours and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis and atherosclerosis), ocular angiogenic diseases (e.g. diabetic retinopathy, corneal graft rejection, etc), cardiovascular diseases, cerebral vascular diseases, diabetes-associated diseases and immune disorders (e.g. chronic inflammation and autoimmunity). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing angiostatin for treating angiogenic diseases involves contacting plasminogen with plasminogen activator and sulfhydryl donor simultaneously, or producing plasmin which is contacted with sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-550019/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2000; 2000US-0500397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 77-80; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soff G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001; 2001WO-US04021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                                                                                                       Fibrinolytic; plasminogen activator; kringle; t-PA; thrombosis; myocardial infarction; cleavage site.
                                                                                                                                                                                                                                                                                                 PA mutant Plg 1-541 [Arg298-299->Gln298-299] t-PA 262-527.
                                                                                                                                                                                                                                                                                                                               31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                       AAR20013 standard; Protein; 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a plasminogen.
                                                                                                                                                      Region
                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                            AAR20013
                                                                                                                                                                                                              Region
               26-MAY-1990;
                                        21-MAY-1991;
                                                                     12-DEC-1991
                                                                                                WO9118989-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 RNPDGDVGGPWCYTTNPRKLYDY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cification describes a method for generating angiostatin in the method comprises contacting plasminogen with a sulfydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gately ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              791 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                               (first entry)
               90GB-0011861
                                          91WO-GB00801
                                                                                                                        /label= t-PA
/note= "[Arg298->Gln, Arg299->Gln]t-PA 262-527
                                                                                                                                                           542..807
                                                                                                                                                                                     /note= "residues
                                                                                                                                                                                                  /label= plasminogen
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Twardowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.18;
95.78;
                                                                                                                                                         domains 1-541, ...
                                                                                                                                            t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 134; DB 22;
Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                      including kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 36
AAR0865
ID AAR08
XX AAR08
XX AAR08
XX Humar
XX Humar
XX Homo
XX Homo
XX Pept
FT Pept
FT Dom
FT PH
FT Dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                  01-MAY-1989;
             (UYNO-) UNIV NOTRE DAME DU
                                                                                                                         15-NOV-1990
                                                                                   26-APR-1990;
                                                                                                                                                              WO9013640-A
                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The fibrinolytic active plasminogen activator (PA) comprises the five kringle domains of plasminogen linked via an amino acid sequence comprising the t-PA cleavage site between residues 275 and 276 and Cy8264 of t-PA, to a t-PA B-chain modified to have a residue other than Arg at position 299. One and two chain variants, Lys/8 and Glul variants and mixt. of these are included.

The PA is used on compsns. to treat thrombotic diseases, in partic. myocardial infarction. Dosage is 0.1-10 (pref. 0.1-2.0) mg/kg by injection for up to 5 doses, or by infusion.
                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human plasminogen; thrombolytic therapy; p119PN127.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR08065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR08065 standard; protein; 810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 30; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hybrid plasminogen activator mutants - useful in treating thrombotic diseases esp. myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-007472/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodd I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BEEC )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 RNPDGDVGGPWCYTTNPRKLYDY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                8908-0345801
                                                                                   90WO-US02296
                                                                                                                                                                                                                   561..810
                                                                                                                                                                                             /label= PMGN PROTEIN PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROUP PLC
                                                                                                                                                                                                                                    (labe)
                                                                                                                                                                                                                                                                                                          'label= KRINGLE_3
                                                                                                                                                                                                                                                                                                                                              label=
                                                                                                                                                                                                                                                                                                                                                                                 'label= KRINGLE_1
                                                                                                                                                                                                                                                                                                                                                                                                                  'label= MATURE_PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= LEADER_SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                         labe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from plasmid p119PN127-6.
                                                                                                                                                                                                                                                                                          . 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%;
95.7%;
                                                                                                                                                                                                                                                     .561
                                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                  L= KRINGLE 5
                                                                                                                                                                                                                                                                     L= KRINGLE_4
                                                                                                                                                                                                                                                                                                                                            KRINGLE_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134; DB 13;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
 RESULT 37
AAR13219
ID AAR13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
WPI; 1991-193201/26.
                                    Castellino FJ,
                                                                       (GETH ) GENENTECH INC
                                                                                                            01-DEC-1989;
                                                                                                                                                 31-OCT-1990;
                                                                                                                                                                                    13-JUN-1991
                                                                                                                                                                                                                        WO9108297-A.
                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R561G human plasminogen variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13219 standard; Protein; 810 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasminogen can be produced by culturing a eukaryotic cell lacking a site-specific plasminogen activator and comprising the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombolytic therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding this amino acid sequence.
Pharmaceutical compsns. containing plasminogen can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression of human plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-361475/48.
N-PSDB; AAQ06648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castellino FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombolytic therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                            89US-0444584.
                                                                                                                                                 90WO-US06345
                                Higgins
                                                                                                                                                                                                                                                                             /label= kringle_5
561..810
                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      whitefleet JL,
                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                               /label= kringle_4
                                                                                                                                                                                                                                                                                                                                                                    /label= kringle_3
                                                                                                                                                                                                                                                                                                                                                                                                         /label= kringle_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= sig_peptide
20..810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= kringle_1
                                                                                                                                                                                                                                                                                                                                                                                           353
                                                                                                                                                                                                                                                                                                                 .561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                263
                                    U
                                                                                                                                                                                                                                                         protein_protease
                                  ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 134; DB 11;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mclinden JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell vector - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Gaps

0;

DЬ Qy

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RESULT 38
AAR12406
ID AAR12
XX AAR12
XX D7 05-SE
XX P1asm
XX P1asm
XX P1asm
XX P1asm
XX P1asm
XX Poote
FT Prote
FT Domai
FT Domai
FT Domai
FT Domai
FT Domai
FT Regic
XX W091c
XX W091c
XX O1-Di
XX GET
XX GET
XX GET
XX GET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid except Lys. Here the amino acids is substituted by early cosition 561 is the critical cleavage site in the conversion of plasminogen to plasmin. The resulting product is proteolytic resistant plasminogen which may be used to treat thrombosis in humans. When complexed with streptokinase, it does not degrade into humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The amino acid at position 475 is Val for the vector pUC119PN127.6, whereas Fig 1 of the specification reflecting the sequence encoding native human plasminogen, contains Ala. The amino acid at 561 of the wild type plasminogen (Arg), is substituted by any amino acid except Lys. Here the amino acids is substituted by 61y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1(A-P); 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human plasminogen variant with replaced ARG-561 - is complexed with fibrinolytic enzyme for use in thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ11998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin and it caused rapid plasminogen activator activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR12406 standard; Protein; 810 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen; proteolytic cleavage; variant; thrombosis; HPg
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R561E human plasminogen variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-1991 (first entry)
 Castellino FJ,
                                                                                                        13-JUN-1991
                                                                                                                                                                       Region
                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1989;
                                                                              31-OCT-1990;
                                                                                                                                                                                                  Domain
                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                      89US-0444584.
                                                                               90WO-US06345
 Higgins D L;
                                                                                                                                                                                                                                                                                                                                     20..810
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                         /label= protein_protease
                                                                                                                                                                                                                                         /label= kringle_3
                                                                                                                                                                                     /label= kringle_5
                                                                                                                                                                                                              /label= kringle_4
                                                                                                                                                                                                                                                                   /label
                                                                                                                                                                                                                                                                                           'label= kringle_1
                                                                                                                                                                                                                                                                                                                      'label= mat_protein
                                                                                                                                                                                                                                                                                                                                               'label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%;
95.7%;
                                                                                                                                                                                                                              .455
                                                                                                                                                                                                                                                        353
                                                                                                                                                                         810
                                                                                                                                                                                                     561
                                                                                                                                                                                                                                                                  kringle_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134; DB 12;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 of the wild-type plasminogen (Arg), is substituted by any amino acid except Lys. Here the amino acids is substituted by Glu. Position 561 is the critical cleavage site in the conversion of plasminogen to plasmin. The resulting product is proteolytic resistant plasminogen which may be used to treat thrombosis in humans. When complexed with streptokinase, it does not degrade into humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-193201/26.
N-PSDB; AAQ11998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The amino acid at position 475 is Val for the vector pUC119PN127.6, whereas Fig 1 of the specification reflecting the sequence encoding native human plasminogen, contains Ala. The amino acid at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmin and it caused rapid plasminogen activator activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1(A-P); 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human plasminogen variant with replaced ARG-561 - is complexed with fibrinolytic enzyme for use in thrombolytic
                                                                                                                                                                                                                                                                                                                                                  plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13220;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13220 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                          R561S human plasminogen variant.
                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                             Homo sapiens
(GETH ) GENENTECH INC
                        01-DEC-1989;
                                              31-OCT-1990;
                                                                    13-JUN-1991
                                                                                           WO9108297-A.
                                                                                                                           Region
                                                                                                                                                   Domain
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                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                        89US-0444584
                                               90WO-US06345
                                                                                                                              561..810
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                              /label= sig_peptide
                                                                                                                                                               /label= kringle_4
                                                                                                                                                                                                            /label= kringle_2
                                                                                                                                                                                                                                                        /label= mat_protein
                                                                                                                                        /label=_kringle_5
                                                                                                                                                                                     'label=
                                                                                                                                                                                                                                  'label= kringle_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%;
95.7%;
                                                                                                                                                                           .455
                                                                                                                                                                                                    .
353
                                                                                                                                                     . 561
                                                                                                                                                                                                                         263
                                                                                                                                                                                      kringle_3
                                                                                                                  protein_protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 134; DB 12; Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 40
AAR13221
ID AAR13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
  01-DEC-1989;
                       31-OCT-1990;
                                                                      WO9108297-A
                                                                                                      Region
                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid at position 475 is Val for the vector pucl19PN127.6, whereas Fig 1 of the specification reflecting the sequence encoding native human plasminogen, contains Ala. The amino acid at 561 of the wild-type plasminogen (Arg), is substituted by any amino acid except Lys. Here the amino acids is substituted by ser. Position 561 is the critical cleavage site in the conversion of plasminogen to plasmin. The resulting product is proteclytic resistant plasminogen which may be used to treat thrombosis in humans. When complexed with streptokinase, it does not degrade into plasmin and it caused rapid plasminogen activator activity.
                                                                                                                             Domain
                                                                                                                                                                        Domain
                                                                                                                                                                                               Domain
                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
                                                                                                                                                                                                                                                                                                                                         Human plasminogen variant.
                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                            AAR13221 standard; Protein; 810
                                                                                                                                                                                                                                                                                                                                                                                        AAR13221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1(A-P); 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human plasminogen variant with complexed with fibrinolytic enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castellino FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ11998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-193201/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                (first entry)
89US-0444584
                       90WO-US06345
                                                                                       /label= protein_protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Higgins D L;
                                                                                                              'label= kringle_5
                                                                                                                                                          /label- kringle_3
                                                                                                                                                                                                                                                /label= sig_peptide
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                              'label= kringle_2
                                                                                                                                                                                                      'label= kringle_1
                                                                                                                                                                                                                          /label= mat_protein
                                                                                                                                   label= kringle_4
                                                                                                                                                 .455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%;
95.7%;
                                                                                                       . 810
                                                                                                                           .561
                                                                                                                                                                                                                    . 182
                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134; DB 12;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replaced ARG-561 - is for use in thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
         Claim 7; Fig 2 and Fig
                              Activatable fibrinolytic and antithrombic proteins - activated e.g. factor {\tt Xa}, thrombin or activated protein C
                                                                       WPI; 1991-208145/28.
N-PSDB; AAQ12547.
                                                                                                              Dawson KM,
                                                                                                                                                                 07-DEC-1989;
07-DEC-1990;
                                                                                                                                                                                                     07-DEC-1990;
                                                                                                                                      (BRBI-) BRIT BIO-TECHN LTD
                                                                                                                                                                                                                                                        WO9109118-A.
                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                               27-JUN-1991.
                                                                                                                                                                                                                                                                                                                              protease; fibrinolysis; blood clotting; thrombosis
                                                                                                                                                                                                                                                                                                                                                       Plasminogen mutein T1 with thrombin cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                              AAR12938;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR12938 standard; Protein; 810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Position 561 is the critical cleavage site in the conversion of plasminogen to plasmin. The resulting product is proteolytic resistant plasminogen which may be used to treat thrombosis in humans. When complexed with streptokinase, it does not degrade
                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmin and it caused rapid plasminogen activator activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid except Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   whereas Fig 1 of the specification reflecting the sequence encoding native human plasminogen, contains Ala. The amino acid at 561 of the wild-type plasminogen (Arg), is substituted by any amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The amino acid at position 475 is Val for the vector pUCl19PN127.6, whereas Fig 1 of the specification reflecting the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1(A-P); 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human plasminogen variant with replaced ARG-561 - is complexed with fibrinolytic enzyme for use in thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castellino FJ, Higgins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1991-193201/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ11998
                                                                                                              Edwards RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                89GB-0027722
90WO-GB01911
                                                                                                                                                                                                     90WO-G001912
                                                                                                                                                                                                                                                                                           Location/Qualifiers 578..580
                                                                                                                                                                                                                                                                              /label= Thrombin cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.18;
95.78;
      5; 73pp; English.
                                                                                                              Forman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134; DB 12;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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AAR34428
AAR34428
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AC AAR3
XX
DT 17-A
XX
Sequ
XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
                                             QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                   Matches
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                  A lambda phage clone comprising a cDNA sequence encoding plasminogen was obtained from Dr. Mark Martsen at the University of Washington. The cDNA was isolated from a human liver library by probing with the partial sequence of Malinowski et al. The sequence of the complete cDNA and the encoded amino acid sequence are shown in AAQ40319 and AAR34428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein is a plasminogen mutant cleavable by thrombin. Activation is localised to the thrombus because cleavage to is by an enzyme of the blood clotting pathway. Compositions comprising the mutant plasminogen are used for treatment or prevention of thrombosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tissue plasminogen activator single chain form fibrinolytic agent - comprises thrombin cleavable zymogen stimulating amido lytic activity, for lysing clots in heart attack and stroke victims and suppressing fibrin matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ40319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5200340-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zymogen; fibrinolytic activity; cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR34428 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 10A, 10B, 10C; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
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532
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RNPDGDVGGPWCYTTNPRKLYDY 554
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22; Conserv
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                                                                                                   Conservative
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95.7%;
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95.78;
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Pred. No. 4.9e-09;
                                                                                                                         Score
Pred.
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                                                                                                                         134; DB 14;
No. 4.9e-09;
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RESULT 43

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AAW31169
AAW31169
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AAW3126
AAW31
                                    This is the protein plasminogen. The encoding cDNA is used in a new process for the production of plasminogen where a first DNA sequence encoding plasminogen and at least one additional DNA sequence encoding a protein that processes or stabilises the plasminogen is introduced into a eukaryotic host cell. The protein is selected from alpha-1-antitrypsin (AAT) and its variants and Argserpins. Both the DNA sequences are operably linked to transcriptional promoter and terminator sequences. The host cell is cultured under conditions that allow the DNA sequences to be expressed and the recombinant plasminogen is isolated from the host cell. Co-expression of plasminogen and the protein gives increased yields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1989;
15-JAN-1988;
28-OCT-1991;
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Misc-difference 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1998
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                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                          Production of recombinant plasminogen - by co-expression
plasminogen-processing or -stabilising protein
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-372063/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-1994;
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                                                                                                                                                                                                                                                                                 2; Fig 6A-D;
                      plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mulvihill
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88US-0144357.
91US-0785865.
94US-0275076.
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel viral gene therapy vector comprising nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector
                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen; human; angiostatin; endostatin; gene therapy; vector;
anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-angiogenic gene therapy vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bachelot T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9926480-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human plasminogen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY08685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY08685 standard;
                                                                                                               532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENETIX PHARM INC. (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                        L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                            RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                     RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-357696/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth;
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leboulch P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0975424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solid tumour; diabetic retinopathy; retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US24950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                    97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pawliuk RJ;
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                    Score 134; DB 20;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134; DB 18;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                               Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 810;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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AAY82690
ID AAY8
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                                                                                                                                               RESULT 46
                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                        Matches
                                                                                                                   AAY82690 standard;
                                                                                                                                                                                                                                                                                                                                            of these properties. The proteins can be used for treating an angiogenic mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatcoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 combinations of angiostatin, endostatin, interferon, thrombospondin, interferon inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiostatin; endostatin; interferon; thrombospondin; interferon inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes multifunctional proteins which comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-255098/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9916889-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor cell production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 77 of WO9916889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 107-109; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolanowski MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY02114 standard; Protein; 810 AA
                                                                                                                                                                                            532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEAR ) SEARLE & CO G D
                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                          1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                     l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                 810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKearn JP;
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97us-0060609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caparon MH,
                                                                                                                   Protein;
                                                                                                                                                                                                                                                                    97.1%;
95.7%;
                                                                                                                   810
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                   Score 134; DB 20;
Pred. No. 4.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casperson GF,
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gregory SA;
                                                                                                                                                                                                                                                                                 Length 810;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                     Gaps
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Human; cathepsin D precursor; PACE4; cancer; metastasis; inhibition; Human plasminogen angiostatin converting enzyme of pH4 (PACE4). 09-AUG-2000 (first entry)

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RESULT 47
AAY53867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                angiogenesis inhibitory protein; vascular endothelial cell; ophtha
                                                            28-MAY-1999;
                                                                                                  02-DEC-1999
                                                                                                                                      W09961464-A1
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                  diabetic
                                                                                                                                                                                                                                                                Human; plasminogen; angiostatin; greenstatin; thrombolytic factor;
                                                                                                                                                                                                                                                                                                        Amino acid sequence of human plasminogen protein.
                                                                                                                                                                                                                                                                                                                                                  13-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                        AAY53867;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY53867 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               part including solid tumours, diabetic retinopathy, and rheumatism. The present sequence represents human plasminogen angiostatin converting enzyme of pH4 (PACE4), which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an enzyme (I) which splits plasma proteins to give fragments which are capable of inhibiting cancer metastasis. (I) has cytostatic, antidiabetic, ophthalmological and antirheumatic activities. (I) splits plasma proteins to produce fragments which can inhibit metastasis. (I) is useful for the treatment and prevention of diseases in which angiogenesis plays a treatment and prevention of diseases in which angiogenesis plays a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzyme useful for treatment and prevention of tumor metastasis other diseases involving angiogenesis, splits plasma proteins tragments capable of inhibiting cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200020570-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasminogen angiostatin converting enzyme of pH4; cytostatic;
antidiabetic; ophthalmological; antirheumatic; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 RNPDGDVGGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-303762/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                              retinopathy; arthritis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaminaka
  98KR-0019535
99KR-0019144
                                                            99WO-KR00263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP05322
                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ζ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takemoto S,
                                                                                                                                                                                                                                otein; proliferation;
ophthalmic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                              810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 134; DB 21;
Pred. No. 4.9e-09;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maeda H,
                                                                                                                                                                                                                            ; angiogenesis; cancer;
glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nozaki C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s
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RESULT 48
AAR12933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the plasminogen protein, specifically angiostatin (comprising amino caids 99-467) and greenstatin (comprising amino acids 101-354) are used cas thrombolytic factors and angiogenesis inhibitory proteins. Angiostatin contains the kringle 1-4 region of plasminogen, and greenstatin contains the kringle 1-4 region of plasminogen, and greenstatin contains contains the kringle 1-3 region of plasminogen. As both proteins contain a high cumber of disulphide bonds, they are difficult to purify. The specification describes a method for the purification of such angiogenesis inhibitory proteins. The method comprises solubilising capacitation of the proteins, produced as inclusion bodies in Escherichia coli and crefolding the solubilised fraction in buffer containing urea and containing urea and containing containing urea and continued that of the proteins are used to suppress inhibitory proteins specifically inhibitory proteins are used to suppress angiogenesis, specifically for treating concerns (e.g. dishetic retinogaths) but also arthritic and accidents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
WPI; 1991-208145/28
                                            Dawson
                                                                                                                                07-DEC-1989;
07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR12933 standard;
                                                                                                                                                                                                 07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen mutein X1 with factor Xa cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR12933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g. glaucoma and diabetic retinopathy), but also arthritis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purifying angiogenesis inhibitors produced 
Escherichia coll, useful as anticancer agen 
diseases
                                                                                      (BRBI-) BRIT
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                                            KM,
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Chang S;
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                                         Edwards RM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 41-45;
                                                                                        BIO-TECHN LTD
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                                                                                                                                89GB-0027722
90WO-GB01911
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                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 578..581 /label= Factor Xa c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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95.7%;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant proteins in and for treating ocular
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RESULT 49
AAR12939
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Best Local :
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This protein is a plasminogen mutant cleavable by Factor Xa. Activation is localised to the thrombus because cleavage to is by an enzyme of the blood clotting pathway. Compositions comprising the mutant plasminogen are used for treatment or prevention of thrombosis, etc.
                                                                                                                                                          Activatable e.g. factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activatable e.g. factor
                                                       is by an enzyme of the blood clotting pathway. comprising the mutant plasminogen are used for prevention of thrombosis, etc. See AAQ12542-Q12558.
                                Sequence
                                                                                                    This protein is a plasminogen mutant cleavable by thrombin. Activation is localised to the thrombus because cleavage to
                                                                                                                                      Claim 7; Fig 2 and Fig 5;
                                                                                                                                                                                             WPI; 1991-208145/28.
N-PSDB; AAQ12548.
                                                                                                                                                                                                                              Dawson
                                                                                                                                                                                                                                                                          07-DEC-1989;
07-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasminogen mutein T2 with thrombin cleavage site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                   811 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrinolytic and antithrombic proteins - activated by \mbox{\sc Xa} , thrombin or activated protein \mbox{\sc C}
                                                                                                                                                           fibrinolytic and antithrombic proteins - \mathbf{Xa}, thrombin or activated protein \mathbf{C}
                                                                                                                                                                                                                              Edwards
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                                                                                                                                                                                                                                                                                                                                                                            /label= Thrombin cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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95.7%;
 97.18;
95.78;
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                                                                                                                                     73pp; English.
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Pred. No. 4.9e-09;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis
                                                                                                                                                                                                                                                                                                                                                                            site
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Search completed: November Job time: 33 secs

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RESULT 50
AAR12943
ID AAR12
XX AAR12
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Matches 22
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                                                                                                                                                                                                                       Activatable fibrinolytic and antithrombic proteins e.g. factor \mathbf{Xa}, thrombin or activated protein \mathbf{C}
                                                                                           Sequence
                                                                                                                             comprising the mutant plasminogen are used for treatment prevention of thrombosis, etc.
                                                                                                                                                   This protein is a plasminogen mutant cleavable by thrombin. Activation is localised to the thrombus because cleavage to is by an enzyme of the blood clotting pathway. Compositions
                                                                                                                                                                                                 Claim 9; Fig 2 and Fig 5;
                                                                                                                                                                                                                                                           N-PSDB; AAQ12552
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07-DEC-1990;
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                                               l Similarity
22; Conserv
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                                              Score 134; DB 12;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein protein search, using sw model

November 8, 2002, 09:31:20; Search time 15 Seconds

(without alignments)
147.337 Million cell updates/sec

Title: Perfect score: US-09-657-431-9 138

RNPDGDVGGPWAYTTNPRKLYDY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
47	48	48	48	48	48	48.5	49	49	49	49	50.5	51	51	51	52	52	53.5	56	56	59
34.1	34.8	34.8	34.8	34.8	34.8	35.1	35.5	35.5	35.5	35.5	36.6	37.0	37.0	37.0	37.7	37.7	38.8	40.6	40.6	42.8
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cell wall-binding	probable plcC prot	2-oxoisovalerate d	hypothetical prote	hypothetical prote	hypothetical prote	plasma membrane H+	ror-related recept	coagulation factor	probable csp prote	polyamine transpor	t-plasminogen acti	carboxylesterase (carboxylesterase (y4hQ protein - Rhi	t-plasminogen acti	hypothetical prote	probable lipoprote	t-plasminogen acti	t-plasminogen acti	neurotrophic recep

ALIGNMENTS

plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A25229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Blol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the A;Reference number: A35229; MUID:90202879

A; Accession: A35229 DNA

A; Molecule type:

A;Residues: 1-810 <PET>

A;Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026 A;Experimental source: leukocyte; lung fibroblast R;Malgaretti, N.; Bruno, L.; PontGglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990 A;Title: Definition of the transcription initiation site of human plasminogen gene in A;Reference number: I52242; MUID:91097523

A;Status: translated from GB/EMBL/DDBJ A; Accession: I52242

A; Molecule type: DNA A; Residues: 1-16 <MAL1>

A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. FEBS Lett. 213, 254-260, 1987

A;Title: Molecular cloning and characterization of a full-length cDNA clone for human A;Reference number: A26646; MUID:87162490 A;Accession: A26646

A; Molecule type: mRNA A; Residues: 1-471,'D',473-810 <FOR>

A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531 A;Experimental_source: liver

R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a A;Reference number: I45961; MUID:85023311

A; Accession: 162738

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 292-471,'D',473-810 <MAL2>

A; Accession: I84609 A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031

A; Status: translated from GB/EMBL/DDBJ

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A: Molecule type: protein
A: Residues: 20-71, E', 73-76 <BRU>
R: Sottrup-Jensen, L:, Petersen, T
submitted to the Atlas, July 1977
A: Reference number: A00929
                                                                                                                                                                                                                                                                                                                                                                                R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J
J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin.
A;Reference number: A58811; MUID:97067211
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J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and A;Reference number: A92458; MUID:85054794
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid
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A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R:Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
submitted to the Brookhaven Protein Data Bank, July 1991
                                 R; Tulinsky, A.; Wu, T.P
                                                        A; Contents: annotation; X-ray crystallography,
                                                                                         submitted to the Brookhaven Protein Data Bank, A; Reference number: A51341; PDB:1PK4
                                                                                                                                                                                                                                                                                   R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, Biochemistry 37, 4699-4702, 1998
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A;Tille: Studies on the active center of human A;Reference number: A92048; MUID:69234739
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A;Residues: 483-507, 'E',509-604 <WI3>
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria,
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A;Title: The primary structure of human plasminogen.
A;Reference number: A92125; MUID:73149248
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Eur. J. Biochem.
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A; Residues: 20-50,'Q',51-71,'E',73-85,87-100
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A;Accession: A04627
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Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments
A;Reference number: S03735; MUID:81212097
                                                                                                                                                            R; Tulinsky, A.; Mulichak, A.M.
                                                                                                                                                                                      A; Contents: annotation
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R.;Biol. Chem. 257, 7401-7406, 1982
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A;Reference number: A92382; MUID:82213905
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                                                                                                                                                                                                                                                         :Title: Generation of an angiostatin-like fragment from plasminogen
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                                                        1.9 angstroms,
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A;Contents: annotation R; Kelley, R.F.; Padmanabhan, K.; R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue A;Reference number: A39483; MUID:92118803
A;Contents: annotation; X-ray crystallography, 2.4 angstroms R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A. submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms
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                                                                                                                                                                                                                                                  C; Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibit C; Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial c
                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation; conformation by (1)H-NMR C; Comment: Plasminogen is synthesized by the kidney and is present in place; C; Comment: Plasminogen is converted to plasmin by plasminogen activators
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Biochemistry 30, 10576–10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined
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A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
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A; Title: The refined structure of the epsilon-aminocaproic
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                                                                                                                                                                                                                 Stromelysin 1 (see PIR: KCHUS1) acts on plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tulinsky, A.;
                                                                                                                                                                                                                     to produce angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Westbrook,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  and many
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A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in ns the walls of the graafian follicle; also activates the urokinase-type plasminogen

C; Superfamily: plasmin; kringle homology; plasminogen-related

protein

A; Pathway: fibrinolysis

C; Function:

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plasmin (EC 3.4.21.7) precursor - rhesus macaque C;Species: Macaca mulatta (rhesus macaque) C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999 C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr F;1-96/Domain: plasminogen-related protein precursor homology <PLPH> F;1-19/Domain: signal sequence *status predicted <SIG> F;20-810/Product: plasminogen *status experimental <PRO> F;20-96/Domain: activation peptide *status experimental <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Rosidues: 1-810 <TOM>
A;Rosidues: 1-810 <TOM>
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precurse C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase E;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
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F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;79-466/Product: angiostatin #status experimental <AST>
                                                                                                  N;Contains: angiostatin; plasminogen C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 20-Sep-191 #sequence_revision 01-Nov-1996 #text_change C;Accession: A38514; S48202; S48203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Rhesus monkey apolipoprotein(a). A;Reference number: A32869; MUID:89174660 A;Accession: B32869
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F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
A; Title: Characterization of the cDNA coding A; Reference number: A38514; MUID:91184812
                                                   R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W. Genomics 8, 49-61, 1990
                                                                                                                                                                                                               plasmin (EC 3.4.21.7) precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;103-181/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-9/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,665,760/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCGI
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                                                                                                                                                                                                                                                                                                                                                            RNPDGDVGGPWCYTTNPRKLFDY 554
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95.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 1;
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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1;
                         for mouse plasminogen and localization of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 810;
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                                                                                                                                       18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A; Molecule type: mRNA
                            A; Molecule type: protein A; Residues: 1-37; 38-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 20-25 <LIJ>
                                                                                                                                                                                                                                                                                                                                  N; Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                         plasmin (EC 3.4.21.7)
                                                                                                                                                                                                                                                                                                                                                                                         в61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F; 20-812/Product:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
  Straub, C.; Kaempfer, U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                               <SCH>
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C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmediately after dissociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation peptide. C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. C;Function:
                                                                                                                                                                                                                                                F;103-181/Domain: kringle homology <KR1>
F;185-62/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
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F;97-581,582-812/Product: plasmin #status predicted <MAT>
F;97-581/Domain: chain A *status predicted <ACH>
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F;1-19/Domain: signal sequence #status predicted <SIG>
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A;Accession: S48202
                                                                                       R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen
A;Reference number: A61545; MUID:89005015
A;Accession: B61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;136.308/Binding site: carbohydrate (Asn) (covalent) #status pred F;466-467/Cleavage site: Thr-Val (Stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status er;624.667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;582-812/Domain: chain B #status predicted <8CH>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335
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                                                                                                                                                                                                                                                                                                                                           N;Contains: miniplasminogen C;Species: Ovis orientalis aries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bonds: #status predicted F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 RNPDGDVNGPWCYTTNPRKLYDY 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor -
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91.3%;
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Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sheep (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Rickli,
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                                                                                                                                                                           of various species
Ħ
                                                                                                                                                                                                                                                                                                              (domestic sheep)
#text_change 17-Mar-1999
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glycoprotein; h
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plasmin (BC 3.4.21.7) precursor - western European hedgehog
C:Species: Erinaceus europaeus (Western European hedgehog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46260
R:Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apc
A;Reference number: I46259; MUID:96025778
A;Accession: I46260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <LAW>
A;Residues: 1-810 <LAW>
A;Cross-references: EMBL:U33171; NID:91046360; PID:91046361
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor
C:Reywords: hydrolase; serine proteinase
F;103-181/Domain: kringle homology <KR1>
F:185-262/Domain: kringle homology <KR2>
F:185-262/Domain: kringle homology <KR2>
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F;379-456/Domain: 1
F;482-561/Domain: 1
F;582-803/Domain: 1
                                                                                               apoprotein(a) (EC 3.4.21.-) precursor [validated] - human N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) G;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000 C;Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286 R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fles: Nature 330, 132-137, 1987
A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen A;Reference number: S00657; MUID:88039109
A;Accession: S00657
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A;Molecule type: protein
A;Residues: I18-460 <SC2>
A;Residues: I18-360 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
F;1-37,38-117,118-460/product: plasminogen (fragments) #status experimental <PRO>
F;1-37/Domain: activation peptide (fragment) #status experimental <APT>
F;38-117,118-230,331-460/product: plasmin (fragments) #status experimental <MAT>
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F;118-460/Product: miniplasminogen #status experimental <MIN>
F;118-460/Product: miniplasminogen #status experimental <MIN>
F;132-211/Domain: kringle homology <KR5>
F;232-460/Domain: plasmin chain B #status experimental <BCH>
F;231-453/Domain: trypsin homology <KRY>
F;272,315,410/Active site: His, Asp, Ser #status predicted
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A;Accession: S28200
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A; Title: Complete amino acid sequence of ovine miniplasminogen
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPDGDANGPWCYTTNPRKLFDY 555
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trypsin homology <TRY>
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kringle homology <KR4>
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82.6%;
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                                                                                                                                 Eaton, D.L.; Chen, E.Y.; Fless, G.M.;
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F:940-1017/Domain: kringle homológy <KR9>
F:054-1131/Domain: kringle homológy <KR10>
F:1168-1245/Domain: kringle homológy <KR11>
F:1282-1359/Domain: kringle homológy <KR12>
                                                                                                                                                                    F;370-447/Domain: kringle homology <KR4>
F;484-561/Domain: kringle homology <KR5>
F;598-675/Domain: kringle homology <KR6>
F;712-789/Domain: kringle homology <KR7>
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A;Tittle: Multiple members of the plasminogen-apolipoprotein(a) gene family associated A;Reference number: I52415; MUID:92207924
A;Accession: I52415
A;Accession: I52415
                                                                                                                                                                                                                                                                                                               F;142-219/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine F;1-19/Domain: signal sequence #status predicted <SIG>
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C; Superfamily: apolipoprotein(a); kringle homology; trypsin homology
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                                                                                                                                           F;826-903/Domain: kringle homology <KR8>
                                                                                                                                                                                                                                                                                                                                                                               F;28-105/Domain: kringle homology <KR1>
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A;Map position: 6q26-6q27
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A;Title: 5' control regions of the apolipoprotein(a) gene and A;Reference number: A47277; MUID:93165698
A;Accession: A47277
                                                                                                                                                                                                                                                                                                                                                                                                               F; 20-4548/Product: apolipoprotein(a) #status
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A; Residues: 1-16 < RE4>
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A; Residues: 1-16 < RE3>
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A; Residues: 1-16 < RE5>
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A; Residues: 1-16 < RE2>
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A; Residues: 1-16 < RES>
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A; Residues: 20-21, 'P', 23-34;177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200;292-314, 'W', 316
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A; Residues: 1-4548 < MCL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       several genes closely linked on chromosome 6 are identical in
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F;1510-1587/Domain: kringle hor F;1524-1701/Domain: kringle hor F;1738-1815/Domain: kringle hor F;1852-1929/Domain: kringle hor F;1852-1929/Domain: kringle hor F;2080-2157/Domain: kringle hor F;2080-2157/Domain: kringle hor F;2194-2271/Domain: kringle hor F;2336-2613/Domain: kringle hor F;2452-2499/Domain: kringle hor F;2536-2613/Domain: kringle hor F;2670-2727/Domain: kringle hor F;2670-3270/Domain: kringle hor F;3320-327/Domain: kringle hor F;3448-3525/Domain: kringle hor F;3448-3525/Domain: kringle hor F;3464-3525/Domain: kringle hor F;3570-3639/Domain: kringle hor F;3570-3753/Domain: kringle hor
                                                                                                                          A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 118-455 <SC2>
G;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Superfamily: plasmin; kringle homology; plasminogen fragments; serine proteinase; z
F;1-33,33-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F:1-33,Domain: activation peptide (fragment) #status experimental <APT>
F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F;37-114/Domain: kringle homology <KR4>
F;118-455/Product: miniplasminogen #status experimental <MIN>
F;226-4455/Domain: kringle homology <KR5>
F;126-205/Domain: kringle homology <KR5>
F;226-4455/Domain: trypsin homology <KR5>
F;226-4455/Domain: trypsin homology <KR5>
F;226-4455/Domain: trypsin homology <KR5>
F;226-4455/Domain: trypsin homology <KR5>
F;267,310,405/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (EC 3.4.21.7) precursor - horse (fragments)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Equus caballus (domestic horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-33;34-117 <SCH>
A;Residues: 1-35;34-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A;Title: Complete amino acid sequence of equine miniplasminogen.
A;Reference number: S17527; MUID:92052077
A;Accession: S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: A61545; S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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F;4328-4541/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;4124-4201/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;4010-4087/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;3782-3859/Domain:
F;3896-3973/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Structural aspects of the plasminogen of various species A; Reference number: A61545; MUID:89005015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A61545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Schaller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzyme 40, 63-69, 1988
   Matches
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4279 RNPDGDINGPWCYTMNPRKLFDY 4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Rickli, E.E.
   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Conservative
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78.3%;
                               82.6%;
78.3%;
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Pred. No. 3.3e-08;
                                   Score 114; DB 2;
Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <KR14>
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       Mismatches
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                                                                      Length 455;
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Eur. J. Blochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen A;Reference number: A25834; MUID:85203907
A;Accession: A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E. Fibrinolysis 1, 91-102, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>F;1-77/Domain: activation peptide #status predicted <APT>F;78-560/Product: plasmin chain A #status predicted <ACH>F;84-162/Domain: kringle homology <KR1>F;84-162/Domain: kringle homology <KR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a ns_the walls_of the graafian follicle; also activates the urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 450-790 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-57 <BRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Blochem. 114, 465-470, 1981
A;Tille: Comparison of the primary structure of the N-terminal CNBr fragments of huma
A;Reference number: S03735; MUID:81212097
A;Accession: S03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S03733
A; Accession: S03733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmin (EC 3.4.21.7) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;450-790/Product: miniplasminogen #status experimental <MIN>F;461-540/Domain: kringle homology <KR5>F;561-790/Product: plasmin chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-560 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
C;Accession: S45046; A25835; I45961; S03736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;256-333/Domain: kringle homology <KR3>F;358-435/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-790/Product: plasminogen #status predicted <PRO>
                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bonds: #status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;561<sup>-</sup>783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;166-243/Domain: kringle homology <KR2>
                                                                                                                            plasmin (EC 3.4.21.7) precursor - bovine
                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 RNPDGDVNGPWCYTMNPQKLFDY 199
                                                                                                                                                                                                                                                                                               512 RNPDGDDNGPWCYTTNPQKLFDY 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.9%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113; DB 1;
pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 790;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
C:Accession: JC5061
                                                                                                             macrophage-stimulating protein 1 precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
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                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <MAT>
F;104-583/Domain: plasmin chain A #status experimental <MAT>
F;104-583/Domain: kringle homology <KRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
F:1-26/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;624,667,762/Active site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;485-564/Domain:
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F;27-812/Product: plasminogen #status experimental <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ns the walls of the graafian follicle; also activates the urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 27-83 <BRU> C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUID:81212097
A;Accession: S03736
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A; Molecule type: mRNA
A; Residues: 706-743, 'R', 745-812 <MAL>
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A; Residues: 27-334,'D', 336-515,'H',517-554,'L',556-812 <SCH>
R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
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A; Accession: I45961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmar. Reference number: A25835; MUID:85203906
A;Accession: A25835
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Eur. J. Biochem. 149, 267-278, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282-359/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-812/Product: plasminogen #status experimental <PRO>
                                                                                                                                                                                                                                                                                                 536 RNPDGDVNGPWCYTMNPRKPFDY 558
                                                                                                                                                                                                                                                                                                                                                                   1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              it is uncertain whether Met-1 or Met-8 is the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-812 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: kringle homology <KR1>
1: kringle homology <KR2>
1: kringle homology <KR3>
1: kringle homology <KR4>
1: kringle homology <KR4>
1: kringle homology <KR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                His, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
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A; Molecule type: protein
A; Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-
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A;Accession: A61395
A; Map position:
                                     A;Cross-references: GDB:128833; OMIM:142408
                                                                                                                A; Gene: GDB:MST1; D3F15S2; DNF15S2; HGFI
                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                          A; Experimental source: plasma
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A;Title: Cloning, sequencing, and expression of human macrophage stimula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Characterization of the DNF15S2 locus on human chromosome 3: identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 18-Jun-1999
C;Accession: A40331; B40331; A47136; A61395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-711 <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-711 <HA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A40331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrophage-stimulating protein 1 precursor - human
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A;Title: Molecular cloning of rat macrophage-stimulating protein and its involvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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A; Residues: 1-716 < OHS>
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A;Accession: JC5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, Exp. Med. 173, 1227-1234, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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kringle homology <KRI4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.A.; Degen, S.J.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.1%;
65.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and expression of human macrophage stimulating protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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duplication; glycoprotein; growth factor; kringle;

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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;19-483/Domain: alpha chain #status predicted <ACH>
F;10-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR3>
F;783-361/Domain: kringle homology <KR3>
F;70-448/Domain: kringle homology <KR4>
F;484-711/Domain: kringle homology <KR4>
F;484-711/Domain: trypsin homology <KR4>
F;484-704/Domain: trypsin homology <TRY>
F;484-704/Domain: trypsin homology <TRY>
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
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A;Accession: B40332
A;Molecule type: mRNA
A;Residues: 1-18,'P',20-716 <DEG2>
A;Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
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Biochemistry 30, 9781-9791, 1991
A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatocyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
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A; Residues: 1-716 <DEG>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
C;Accession: A35644; S13211
C;Accession: A35644; S13211
R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                       N; Alternate names: hepapoietin A; scatter factor
                                                                                                                                                                                                                                                                                                                A35644
                                                                                                                                                                                                                                                      hepatocyte growth factor precursor - rat
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65.2%;
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Pred. No.
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Pred. No. 3.9e-05;
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                          S.; Nakamun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114;
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                                                                    R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growt
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S. submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: JH0579; MUID:91340155
A;Accession: JH0579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 102, 213-219, 1991
A; Title: Organization of the human hepatocyte growth factor-encoding gene
                          A; Reference number: A41140; MUID: 91334393
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-481, 'RT', 484-728 <SE2>
                                                                                                                                                                                                                                                                                                                A; Accession: JU0333
                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: JU0333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: hepapoietin A; scatter factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatocyte growth factor precursor [validated] - human
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T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, 2, 213-219, 1991

A37796;

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Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of
A;Reference number: A35644; MUID:90222197
A;Accession: A35644
                                                                                                                                                                                                                                                                                                                                                                                                               F:56-495/Product: hepatocyte growth factor #status predicted <MAT>
F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:316-384/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR4>
F:496-728/Domain: kringle homology <KR4>
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F:496-719/Domain: trypsin homology <TRY>
F:496-719/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
C;F1-32/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA
A;Reference number: S13211; MUID:91031482
A;Accession: S13211
                                                                                                                                                                                                                                                                                                        F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predic F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) *status predicted F;488-607/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-728 < OKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D90102; GB:M32987; NID:9220766; PIDN:BAA14133.1; PID:9220767
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                            Matches
                                                                                                                                                                                                                                  Query Match
442 RNPDDDAHGPWCYTGNPLVPWDY 464
                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-728 <TAS>
                                                                                                                                                                Conservative
                                                                                                                                                                                                     60.9%;
                                                                                                                                                                                                                                          59.4%;

    Mismatches

                                                                                                                                                                                                         Pred. No. 0.0006;
                                                                                                                                                                                                                                          Score 82;
                                                                                                                                                                                                                                                  DB 1; Length 728;
                                                                                                                                                                            0;
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R;M1yazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Biochem. 197, 15-22, 1991
                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-288, 'ET' <HAR>
                                                                                                                                                                                                                                                                                                                                                         A;Note: part of this sequence, including the amino end of both the alpha and beta chains R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'Y',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: PH0114; MUID:91207365
A; Accession: PH0114
A; Molecule type: protein
A; Residues: 32-43;53-58 < YOS>
A; Experimental source: plasma
B; Weidner; K.M.; Behrens; J.; Vandekerckhove, J.; Birchmeier; W.
J. Cell Biol. 111, 2097-2108, 1990
                                                                                                                           A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
                                                                                                                                                                                                                                                                                                                                            A; Reference number: I59214; MUID: 9308757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,
R; Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; T.
Nature 342, 440-443, 1989
                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: S06794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A37796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Cell Biol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;YOShiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama, Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy A;Reference number: A39006; MUID:91110540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac A;Reference number: A33512; MUID:89392017
A;Accession: A33512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: embryonic lung
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A; Residues: 1-161, 167-728 < RUB>
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A; Residues: 1-728 <MIY>
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R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, N
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor, Reference number: A36677; MUID:91025062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: leukocyte
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A; Residues: 1-728 <SE3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the authors translated the codon CAG for residue 727 as Glu
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A;Reference number: A60185; MUID:90377927 A;Accession: A60185
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A;Title:

An alternatively processed mRNA generated from human hepatocyte growth factor

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R;Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D. Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
A;Title: Purified scatter factor stimulates epithelial and vascular endothelial cell
                                                                                                                                                                                                                                                                A;Cross-references: GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436 A;Experimental source: fibroblast, COS-1 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: hepapoletin A; scatter factor C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000 C;Date: 03-Mar-1193 #sequence_revision 26-May-1994 #text_schange 16-Jun-2000 C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; JU0231 R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
                                                                                 R; Rosen, E.M.; Meromsky, L.;
                                                                                                                        A; Molecule type: protein A; Residues: 496-504 <SA2>
                                                                                                                                                                                                  A; Accession: PC2064
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-728 <SAS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as
A;Reference number: JC2117; MUID:94183257
                                                                                                                                                                                                                                         A; Note: submitted
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(;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F;1-31/Domain: signal sequence #status predicted <5/16>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F;32-494/Domain: alternative experimental <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC2117
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A:Map position: 7921.1-7921.1

A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1;

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatocyte growth factor precursor - mouse
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F;391-469/Domain: kringle homology <KR4>
F;495-728/Domain: beta chain #Status experimental <BCH>
F;495-716/Domain: trypsin homology <TRY>
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F;211-288/Domain:
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A; Residues: 161-166 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-288, 'ET' <MIY2>
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A;Accession: S15443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 RNPDDDAHGPWCYTGNPLIPWDY 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kringle homology <KR1>
kringle homology <KR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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A;Molecule type: protein
A;Residues: 'X',184-186, 'KX',191-192, 'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,'
R;Liu, Y., Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A;Reference number: S43416; MUID:94060105
A;Accession: S43416
A;Status: preliminary
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A; Reference number: S45521
A; Accession: S45521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 496-517, 'T', 519 <COF>
R; Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 278, 35-41, 1991
A; Title: Purification and characterization of biologically active scatter factor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X72307
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A; Residues: 1-728 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: does not have proteinase activity
(;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
(;Superfamily: hepatocyte growth factor; heterodimer;
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;
F;1-32/Domain: signal sequence #status predicted <SIC>
F;1-32/Domain: signal sequence #status predicted <SIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-30 <RES>
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A; Accession: $10966
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                                                                                                                                                                                                                                                           F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted F;488-607/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: I48758; MUID:95122532
A; Accession: I48758
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A; Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 < NAT>
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В
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                                                                                                                                                                                                 Query Match
442 RNPDDDAHGPWCYTGNPLIPWDY 464
                                                                                                                                                                       Local Similarity
                                                                 1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              kringle homology <KR2>
kringle homology <KR3>
kringle homology <KR4>
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                                                                                                                                                                    58.7%;
60.9%;
                                                                                                                                                                       Score 81; DB 1; Pred. No. 0.00084;
                                                                                                                                          Mismatches
                                                                                                                                          8
                                                                                                                                                                                                        Length 728;
                                                                                                                                              0;
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kringle;
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RESULT 16

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thrombin (EC 3.4.21.5) precursor - bovine (Species: Bos primigenius taurus (cattle) (Species: Bos primigenius taurus (cattle) (C;Pate: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999 (C;Pate: 24-Apr-1984 #sequence_18.37552; 146045; S67518 (C;Paccession: S02537; A00915; A37552; 146045; S67518 R;Irwin, D.M.; Robertson, K.A.; MacGillivray, R.T.A. J. Mol. Biol. 200, 31-45, 1988
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A; Note: disulfide bonds and carbohydrate binding sites were determined
R; Park, C.H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
A; Fitle: Three-dimensional structure of the kringle sequence: structure of prothrombi
A; Reference number: A37553; MUID: 86296631
A; Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
R; Irwin, D.M.; Ahern, K.G.; pearson, G.D.; MacGillivray, R.T.A.
Biochemistry 24, 6861-6861, 1985
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A;Contents: annotation; gene structure
R;MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A;Title: Cloning and analysis of a cDNA coding for bovine prothrombin. A;Reference number: 146045; MUID:81054926
A;Accession: I46045
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Biochemistry 23, 1626-1634, 1984
A;Title: Characterization of bovine prothrombin mRNA and its translation product.
A;Reference number: A00915; MUID:84203525
A;Accession: A00915
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A; Accession: S02537
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A; Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625
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A; Residues: 1-230,'H',232-625 <MAC>
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A; Residues: 1-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: thrombin; Gla domain homology; Killigle Homology; C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl C;Keywords: blood coagulation; calclum binding; carboxyglutamic acid; duplication; gl F;1-24/Domain: signal sequence #status predicted <SIG>
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A; Residues: 318-325;333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
C; Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi
C; Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi
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A;Cross-references: EMBL:V00135, NID:9772; PIDN:CAA23451.1; PID:9808945
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                                                                                                                F;44-625/Product: prothrombin #status experimental <MPT>
F;44-199/Domain: activation peptide 1 #status experimental <FR1>
F;109-187/Domain: kringle homology <KR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: The prothrombin precursor is synthesized in the liver. C;Superfamily: thrombin; Gla domain homology; kringle homology; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb ent interaction with the negatively charged phospholipid membrane surface.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tivation peptide and cleaves the remaining part into light and heavy chains. The acti
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Eur. J. Biochem. 227, 102-107, 1995
_{\rm F;210-317/Domain:} activation peptide 2 _{\rm F;214-292/Domain:} kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                F;25-43/Domain: propeptide *status predicted <PRO> F;28-88/Domain: Gla domain homology <GLA>
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                                                                          activation peptide 2 #status experimental <FR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin homology
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A;Cross-references: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933
A;Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor R;Description: stimulates mitosis of hepatocytes and other cells
C;Function:
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
E;42-477,478-709/Product: hepatocyte growth factor #status predicted <ACH>
E;42-477,70main: hepatocyte growth factor alpha chain #status predicted <ACH>
E;115-193/Domain: kringle homology <KR2>
E;189-367/Domain: kringle homology <KR2>
E;289-367/Domain: kringle homology <KR2>
E;289-367/Domain: kringle homology <KR4>
E;478-709/Domain: kringle homology <KR4>
E;478-709/Domain: kringle homology <KR4>
E;478-709/Domain: kringle homology <KR4>
                         A;Reference number: A40522; MUID:91250378
A;Accession: A40522
A;Status: preliminary
                                                                                                                                                                                    Clasmin (EC 3.4.21.7) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: A40522
R;Kanalas, J.J.; Makker, S.P.
                                                                                                    R;Kanalas, J.J.; Makker, S.P.
J. Biol. Chem. 266, 10825-10829, 1991
A;Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
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F;478-700/Domain: trypsin homology <TRY>
F;528,128,881,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-710 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C;Accession: I51283
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F:50.51.58.60.63.64.69.70.73.76/Modified site: gamma-carboxyglutamic acid (Glu) #status F:61-66.91-104.109-187.130-170.158-182.214-292.235-275.263-287.339-485.394-410.539-553.5 F:120.144.419/Binding site: carbohydrate (Asn) (covalent) #status experimental F:409.465.571/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I51283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: hepapoietin A; scatter factor C;Species: Xenopus sp. (clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             470-588/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RNPDGDVGGPWAYTTNPRKLYDY 23
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70.6%;
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Pred. No. 0.0022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                          189 RNPDQDPQGPWCYTXNP 205
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A;Molecule type: protein
A;Rosidues: 1-15;16-34;35-44;45-59;60-76;77-111;111-138;139-158;159-178;179-216;217-2
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol F;81-146/Domain: kringle homology <KR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gher Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node du A;Reference number: I51285; MUID:95237013
                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Petromyzontidae gen. sp. (lamprey)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 07-Nov-1997
C;Accession: S33879
                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                   A; Accession: S33879
                                                                                                                                                                                                                                                                                                         A; Title: Isolation, characterization
                                                                                                                                                                                                                                                                                                                                  R;Affolter, M.; Schaller, J.; Rickli, Protein Seq. Data Anal. 5, 207-211, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmin precursor - lamprey (fragments)
N;Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S33879
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C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F:124-197/Domain: kringle homology <KRG>
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A;Cross-references: GB:M62832; NID:g206215; PIDN:AAA41884.1; PID:g554488
A;Cross-references: GB:M62832; NID:g206215; PIDN:AAA41884.1; PID:g554488
A;Note: the authors translated the codon TCT for residue 76 as Ala
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;34-112/Domain: kringle homology <KRG>
F;34-112,75-95,83-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                    A; Reference number: S33879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
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A; Residues: 1-411 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: 151285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatocyte growth factor/scatter factor - chicken (fragment)
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                                                  Matches
                                                                                             Query Match
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                                                                        Local
1 RNPDGDVGGPWAYTTNP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYD 22
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                                             12;
                                                                      Similarity
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                                               Conservative
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kringle homology <KR2>
                                                                 52.9%;
70.6%;
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50.0%;
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                                                                 Pred
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                                                              Score 73; DB 2;
Pred. No. 0.0053;
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                                          Mismatches
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                                                                                                                                                                                                                                                                                                 partial amino acid sequence of lamprey plasm
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                                                                                     Length 336;
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                                     Gaps
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thrombin (EC 3.4.21.5) B chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 22-Jun-1999
C;Accession: S10511; A60576; B42696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 383-617, 'E' <BAN>
A; Cross-references: GB:M81397
C; Superfamily: thrombin; Gla
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A; Accession: A60576
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;215-292/Domain: kringle homology <KR2>F;360-609/Domain: trypsin homology <TRY>F;360-609/Domain: trypsin homology <TRY>F;560,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5;402,458,564/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-43/Domain: propeptide #status predicted <PRO>
F;25-43/Domain: Gla domain homology <GLA>
F;28-88/Domain: Gla domain #status experimental <PMAT>
F;109-187/Domain: kringle homology <KRl>
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A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and
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                                                                                                                                                                                       R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot A;Reference number: 146259; MUID:96025778
A;Accession: T18518
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Erinaceus europaeus (Western European hédgehog)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C;Accession: T18518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apolipoprotein(a) - western European hedgehog (fragment)
                                    A; Experimental source: liver C; Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis,
                                                                                                 A;Molecule type: mRNA
A;Residues: 1-2869 <LAW>
A;Cross-references: EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC48522.1
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ent apolipoprotein(a).
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52.5%;

Score 72.5;

DB 2;

Length 2869;

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A;Cross-references: GB:x52308; NID:g53813; PIDN:CAA36548.1; PID:g53814
A;Experimental source: strain C57BL/6
A;Experimental source: strain c57BL/6
A;Oncte: the data were obtained from females resulting from the cross of M. domesticus R;Danfield, D.K.; MacGillivray, R.T.A.
R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification amplification and A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification amplication amplification amplification amplification ampli
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C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 22-Jun-1999
C;Accession: A35827; A42696; S12081
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C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-43/Domain: propeptide #status predicted <PRO>
F;28-88/Domain: Gla domain homology <GLA>
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F;109-187/Domain: kringle homology <KR1>
F;215-293/Domain: kringle homology <KR2>
F;215-293/Domain: kringle homology <KR2>
F;361-610/Domain: trypsin homology <TRY>
F;30,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54
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A; Residues: 1-618 <DEG>
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DNA Cell Biol. 9, 487-498, 1990
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A; Residues: 384-618, 'E' <BAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C;Accession: A29351; A00914; B00914; A37549; A37550; 151952
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                                                                                                                                                                                                 A;Title: Nucleotide sequence of the gene for human prothrombin A;Reference number: A29351; MUID:88077877 A;Accession: A29351
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A;Molecule type: DNA A;Acsidues: 1-622 <DEG> A;Residues: 1-622 <DEG> A;Cross:references: GB:M17262; GB:M33691; NID:g558069; PIDN:AAC63054.1; PID:g339641 R;Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
                                                                                                                                                                                                                                                                                                                                                    R; Degen, S.J.F.; Davie, E.W.
Biochemistry 26, 6165-6177, 1987
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64.7%;
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Pred. No. 0.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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F;108-186/Domain: kringle homology <KR1>
F;213-291/Domain: kringle homology <KR2>
F;213-291/Domain: kringle homology <KR2>
F;328-363/Product: thrombin light chain #status experimental <LCH>
F;364-612/Product: thrombin heavy chain #status experimental <HCH>
F;364-613/Domain: trypsin homology <TRY>
F;49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status F;60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336-482,536-559,564-594/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 11p11-11q12
A; Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
E; 1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:33031; NID:g190723; PIDN:AAA60220.1; PID:g190724
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibri
C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
) can be removed either by factor Xa or thrombin; the cleavage into light and heavy chai
ter 314-Arg, are released in natural blood clotting.
C;Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C;Comment: The prothrombin precursor is synthesized in the liver.
                                                                                                                                              F;416/Binding site: carbohydrate (Asn) (covalent) *status experimental F;568/Active site: Ser *status experimental
                                                                                                                                                                                                                              F;406,462/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;25-43/Domain: propeptide #status predicted <PRO> F;28-87/Domain: Gla domain homology <GLA> F;44-622/Product: prothrombin #status experimental <MAT>
                                                                                                                                                                                                                                                              F;391-407/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;44-327/Domain: activation peptide #status experimental <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:F2
A;Cross-references: GDB:119894; OMIM:176930
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A;Title: Recombinant genetic approaches to functional mapping of thrombin. A;Reference number: I51952; MUID:87182874
A;Accession: I51952
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A:Residues: 315-334,'N',336-348,'N',350-368,'N',370-397,'N',399-413,'N',415-484,'N',486-R:Rablet, M.J.; Blashill, A.; Furie, B.; Furie, B.C.
J. Biol. Chem. 261, 13210-13215, 1986
A:Reference number: A37551; MUID:87008532
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A; Residues: 1-2, 'RI', 5
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A:Residues: 44-118,'N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,

R:Butkowski, R. J.; Elion, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A:Title: Primary structure of human prethrombin 2 and alpha-thrombin.

A:Reference number: A37550; MUID:77207112
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A;Accession: A00914
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A; Residues: 188-311 <DE3>
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                       Matches
                                                                                               Query Match
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                                                       Local Similarity
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               Conservative
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                                                   64.78;
                                       Score 71;
Pred. No.
       Mismatches
                                       0.021;
                                                                           DB 1; Length 622;
       Indels
0;
Gaps
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C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999 C;Accession: A32869; A30848 R;TomLinson, J.E.; McLean, J.W.; Lawn, R.M. J. Biol. Chem. 264, 5957-5965, 1989
A; Title: Rhesus monkey apolipoprotein(a). A; Reference number: A32869; MUID:89174660
                                                                                                                                                  C; Species: Macaca mulatta (rhesus macaque)
                                                                                                                                                                       apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;6-83/Domain: kringle homology <KRG>F;6-83/27-66,55-78/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gyenes, M.; Patthy, L.
Biochin. Biophys. Acta 832, 326-330, 1985
A;Title: The kringle 4 domain of chicken r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-89 <GYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A60140; MUID:86077796
A;Accession: A60140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (EC 3.4.21.7) precursor - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;41-118/Domain: kringle homology
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A;Accession: C61545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-123 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmin (EC 3.4.21.7) precursor - goat (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 RNPDAD-KSPWCYTTDPRVRWEF 112
                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPWAYTTNPRKLYDY 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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52.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66.5;
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Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                  Sequence, evolution, and sites of synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.011;
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-120 <SCH>
A; Residues: 1-120 <SCH>
C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C; Keywords: hydrolase; serine proteinase
F; 37-114/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv1490 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70711
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmin (EC 3.4.21.7) precursor - dog (
N;Alternate names: plasminogen
C;Species: Canis lupus familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;278-355/Domain: kringle homology <KR3>
F;392-469/Domain: kringle homology <KR4>
F;506-583/Domain: kringle homology <KR5>
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A;Residues: 1-1420 <TON>
A;Cross-references: GB:J04635; NID:g342072; PIDN:AAA36833.1; PID:g342073
C;Superfamily: apolipoprotein(a); kringle homology: trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
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C;Accession: E61545
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F;164-241/Domain: kringle homology <KR2>
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A; Molecule type: mR
                                                                                                                                                                      A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
A;Accession: E70711
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                                                                                                                                                                                                                                                                                                                                                     Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                  A; Residues: 1-435 <COL>
                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Cross-references: GB:Z79701; GB:AL123456; NID:g3261635; PIDN:CAB02040.1; PID:g1524237
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47.8%;
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                                                                                       R; NY, T.
DNA 7, 6
                                                                                                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Se
C;Accession: A35029; A31597
R;Feng, P.; Ohlsson, M.; Ny, T.
J, Biol. Chem. 265, 2022-2027, 71990
A;Title: The structure of the TATA-less rat
A;Reference number: A35029; MUID:90130448
A;Accession: A35029;
A;Accession:
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A; Residues: 1-559 <FEN>
A; Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226
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A; Title: Cloning and characterization of a A; Reference number: A31597; MUID: 89170114
                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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T; Leonardsson, G; 671-677, 1988

Hsueh, A.J.W.

CDNA

rat tissue-type plasminogen activ

10-Sep-1999

#text_change 10-Sep-1999

tissue-type plasminogen activator gene.

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A;Cross-references: GDB:136454
A;Map position: 6p21-6p21
C;Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology;
C;Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; t)
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-937/Product: neurotrophic receptor ror2 #status predicted <MAT>
F;36-137/Domain: immunoglobulin homology <IMM>
F;36-1394/Domain: kringle homology <KRG>
F;316-394/Domain: kringle homology <IMM>
F;316-394/Domain: kringle homology <KRG>
F;316-394/Domain: kringle homology <KRG>
F;316-394/Domain: kringle homology <IMM>
F;316-3
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A; Residues: 1-943 <MAS>
A; Cross-references: GB:M97639; NID:g337466; PIDN:AAA60276.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:120918)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Masiakowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-2619, 1992
A;Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A;Reference number: A45082; MUID:93100347
A;Accession: B45082
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;471-753/Domain: protein kinase homology <KIN>F;479-487/Region: protein kinase ATP-binding motif F;70,188,318/Binding site: carbohydrate (Asn) (covalent) #status
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C; Superfamily:
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t-plasminogen activator (EC 3.4.21.68) precursor -
                                           A35029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59; L
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 2; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID: 9337467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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F:309-553/Domain: trypsin homology <TRY>
F:309-553/Domain: trypsin homology <TRY>
F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-
F:149.481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355,404,510/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;124-205/Domain: kringle homology <KR1>
F;213-294/Domain: kringle homology <KR2>
F;313-294/Domain: kringle homology <KR2>
F;309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
F;309-559/Domain: trypsin homology <TRY>
F;389-583/Domain: trypsin homology <TRY>
F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4
F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;308-309/Cleavage site: Arg-Tle (plasmin, trypsin) #status predicted
F;355,404,510/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                       F;18-29/Domain: propeptide #status predicted <PRO>
F;30-559/Product: t-plasminogen activator #status predicted <MAT>
F;30-308/Product: t-plasminogen activator chain A #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase F;1-17/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A31597
A;Accession: A31597
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-379', K', 381-559 <NYT>
A;Cross references: GB:M23697; NID:q530159; PIDN:AAA41812.1; PID:q530160
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-29/Domain: propeptide #status predicted <PRO>
                                                                                                                                                                                     F;309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
                                                                                                                                                                                                                              F;83-116/Domain: EGF homology <EGF>
F;124-205/Domain: kringle homology <KR1>
F;213-294/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 33-37, 'X', 39-40 <LIW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J03520; NID:g202109; PIDN:AAA40470.1; PID:g202110 R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263, 1563-1569, 1988
A;Title: Molecular cloning of complementary DNA to mouse tissue
A;Reference number: A29941; MUID:88087303
                                                                                                                                                                                                                                                                                                                                                   F;38-75/Domain: fibronectin type I repeat homology <1F1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 33-37, 'X', 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S48202; MUID:95010076 A; Accession: S48205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-559 < RIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A29941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  t-plasminogen activator (EC 3.4.21.68) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
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F;30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F;38-75/Domain: fibronectin type I repeat homology <1Fl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A29941; S48205; S48207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 RNPDGD-AKPWCHVMKDRKLTWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           predicted <ACH>
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A; Map position:
A; Introns: 104/2
C; Superfamily: C
DЬ
                                 QΥ
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A; Residues: 1-323 <WIL>
                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z19980
A; Accession: T25094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γQ
                                                                                                                                                                                                         A; Gene:
                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                               A; Experimental source: clone T22A3
                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z81125; PIDN:CAB03383.1;
                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                 R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T22A3.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL031514; PIDN:CAA20597.1; GSPDB:GN00070; SCOEDB:SC2H4.03
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A; Residues: 1-153 <OLI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T37219
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14
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                                                                                          Local
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                                                                                                                                                                                                         CESP: T22A3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCOEDB: SC2H4.03
RNPDKNPLGPWCYVGN
                                 RNPDGDVGGPWAYTTN 16
                                                                                                                                        104/2; 136/2; 226/3; 242/2
ily: Caenorhabditis elegans hypothetical protein T22A3.6
                                                                       l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     T25094
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                         37.7%;
56.2%;
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%;
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                                                                                                        Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53.5; D
Pred. No. 1.6;
                                                                                         Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB Pred. No. 2.9;
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                                                                       Mismatches
                                                                                                            DB 2;
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                                                                                                        Length 323;
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C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human N;Alternate names: t-PA; tissue plasminogen activator

UKHUT

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A; Residues: 31-562 <ITA>
A; Cross-references: DDBJ:D01096; NID:9220128; PIDN:BAA008B1.1; PID:9441174
A; Cross-references: DDBJ:D01096; NID:9220128; PIDN:BAA008B1.1; PID:9441174
A; Experimental source: embryonic lung fibroblast IMR-90 cells
A; Note: part of this sequence, including the amino end of the mature protein, was confir R.Pennica, D; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett Nature 301, 214-221, 1983
A; Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Eschela, Accession: A93293; MUID:83115262
A; Accession: A93293; MUID:83115262
A; Residues: 1-562 <PEN>
A; Residues: 1-562 <PEN>
A; Cross-references: GB:L00141
A; Experimental source: melanoma cells
R; Sasaki, H; Saito, Y; Hayashi, M; Otsuka, K; Niwa, M.
Nuclecic Acids Res. 16, 5695, 1988
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J. Biol. Chem. 261, 6972-6985, 1986
A;Title: The human tissue plasminogen activator gene.
A;Reference number: A23529; MUID:86196143
A;Recession: A23529
A;Mocession: A23529
A;Molecule type: DNA
A;Residues: 1-562 cDEG>
A;Residues: 1-562 cDEG>
A;Rossereferences: GB:K03021; NID:9339817; PIDN:AAA98809.1; PID:9339818
R;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
Agric. Biol. Chem. 55, 1225-1232, 1991
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A;Accession: A91343
A;Molecule type: mRNA
A;Experimental source: Detroit 562 cells; ATCC 138
A;Experimental source: Detroit 562 cells; ATCC 138
R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
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A;Title: The structure of the human tissue-type plasminogen
A;Reference number: A94004; MUID:84298137
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S. Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen A;Reference number: A93951; MUID:83169656
A;Accession: A93951
A;Molecule type: mRNA
A;Residues: 251-358 <EDL>
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A; Residues: 1-562 < NYT>
                                                                     R; Pohl, G.; Kaplan, L.; Ein: FEBS Lett. 168, 29-32, 1984
                                                                                                                                                                                                                                                                                                              A; Experimental source: melanoma cells R; Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, Biochemistry 23, 3701-3707, 1984
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A;Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244
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                                                                                                                                                                                                A; Reference number: A90488; MUID: 85000468
                                                                                                                                                                                                                                             differences
                                                                                                                                                                                                                                                                     A; Title: Tissue plasminogen activator: peptide
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    A; Reference number:
                                        A; Title: Differences between uterine and melanoma
                                                                                                                                                   A; Contents: annotation; melanoma cells,
A91322; MUID:84158956
                                                                                                              Einarsson, M.; Wallen,
                                                                                                                                                       partial sequence of residues 36-562, active
                                                                                                                                                                                                                                                                          analyses confirm an indirectly derived
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                                        forms of tissue
                                                                                                                  Jornvall,
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                                    plasminogen activator
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S02125; A91343; A93951; A91322; A54645;
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                                                                                                                                                                                                     F;127-208/Domain: kringle homology <kR1>
F;215-296/Domain: kringle homology <kR2>
F;215-296/Domain: kringle homology <kR2>
F;311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
F;311-566/Domain: trypsin homology <TRY>
F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,29
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A:Map position: 8p12-8p12

A:Map position: 8p12-8p12

A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3;

A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3;

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase C;Keywords: signal sequence #status predicted <SIG>

F;1-23/Domain: signal sequence #status predicted <SIG>
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A;Title: Isolation and characterization of the human tissue-type plasminogen A;Reference number: I55232; MUID:85289338
A;Accession: I55232
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Thromb. Haemost. 59, 523-528, 1988
A;Title: Isolation, identification and pharmacokinetic properties of A;Reference number: A60902; MUID:89044681
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A; Molecule type: pro
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A;Accession: I60110
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A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its
A;Reference number: A54645; MUID:86284200
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EMBO J. 5, 3525-3530,
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A; Reference number: A37567; MUID:87033611
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A; Residues: 33-45; 311-320 < POH>
                                        F;152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental F;219/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F;319-311/Coleavage site: Arg-Iie (plasmin, trypsin) #status experimental F;357,406/Active site: His, Asp #status predicted
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F;33-310/Product: t-plasminogen activator chain A #status experimental <ACH>
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A; Residues: 1-562 <HAR>
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F;357,406/Active site: His, Asp #status pre F;513/Active site: Ser #status experimental
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A; Residues: 1-562 < RES>
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525-3530, 1986
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carboxylesterase (EC 3.1.1.1) FE4 precursor - green peach aphid
C;Species: Myzus persicae (green peach aphid)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S36787
R;Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
                                                                                                 RESULT 38
S36787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxylesterase (EC 3.1.1.1) E4 - green peach aphid C;Species: Myzus persicae (green peach aphid) C;Date: 09-Jun-1994 #sequence_revision 01-Dec-1995 #text_change C;Accession: S36786 R;Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L. Biochem. J. 294, 569-574, 1993
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                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X74554; NID:g397510; PIDN:CAA52648.1; C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase C;Keywords: carboxylic ester hydrolase F;52-552/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S36786; MUID:93384534
A; Accession: S36786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 294, 569-574, 1993
A:Title: Cloning and analysis of the esterase genes conferring
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A;Title: Molecular basis of symbiosis between Rhizobium and legumes.
A;Reference number: Z14734; MUID:97305956
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-552 <FIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDB.
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C; Accession:
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42.1%;
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72.7%;
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45.8%;
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Pred. No.
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Pred. No.
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10-Sep-1999 #text_change 10-Sep-1999
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1.9;
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C;Accession: B83194
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, I.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

hi, S.D.; Warrener, Folger, K.R.; Kas,

Α . . .

Hickey, Larbig,

X X

рa

polyamine transport protein PotB PA3608 [imported] - Pseudomonas aeruginosa C_7 Species: Pseudomonas aeruginosa

(strain

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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

A; Reference number: A82950; A; Accession: E83194

A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A; Reference number: A82950; MUID: 20437337

A;Status: preliminary

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A;Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g166079
A;NOte: the authors translated the codon ATC for residue 75 as Thr
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
E;1-21/Domain: signal sequence #status predicted <SIG>
F;22-36/Domain: propeptide #status predicted <PRO>
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                                                                                                                                                                                                   F;142-143/Cleavage site: His-Ser (plasmin) #status predicted F;189,238,345/Active site: His, Asp, Ser #status predicted F;315/Binding site: carbohydrate (Asn) (covalent) #status pro
                                                                                                                                                                                                                                                                          F;37-394/Product: plasminogen activator gamma #status predicted <PLA>
F;45-126/Domain: kringle homology <KRG>
F;143-388/Domain: trypsin homology <TRY>
F;45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bond
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A;Title: Cloning and analysis of the esterase genes conferring insecticide resistance A;Reference number: S36786; MUID:93384534
A;Accession: S36787
Вþ
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A; Residues: 1-394 < KRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
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Gene 105, 229-237, 1991
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                                                                                                                               Query Match
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RNPDG-ASKPWCYVIKARK 115
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8; Conserv
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42.1%;
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Pred. No. 13;
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A;Residues: 1-297 <STO>
A;Cross-references: GB:AE004781; GB:AE004091; NID:g9949761; PIDN:AAG06996.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: potB; PA3608
C;Superfamily: spermidine/putrescine transport system permease protein potH
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho; Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 30-Jun-1991 #text_change 08-Dec-2000
C;Accession: A29411; A26814; A00930; A25191; A22248; A21037
R;Cool, D.E.; MacGillivray, R.T.A.
J;Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon A;Reference number: A29411; MUID:88007593
A;Accession: A29411; MUID:88007593
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A;Accession: G70520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M17466; GB:J02807; NID:g180355; PIDN:AAB59490.1; PID:g180357 R;Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R. Nucleic Acids Res. 14, 3146, 1986
A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).
A;Reference number: A26814; MUID:86176794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human N; Alternate names: Hageman factor (activated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: csp
                          A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 4-615 < TRI>
A; Residues: 4-615 < TRI>
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M312291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M312291; PIDN: AAA70225.1; PID: 9182292
A; Cross-references: GB: M312292
A; Cross-references: GB: M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-615 < COO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFHU12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 42
A; Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the
                                                                                                                                                                                                                                                                                                        A; Accession: A26814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNPDGDVGGPW---AYTTNPR 18
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45.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred
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                          ror-related receptor RTK - Pacific electric ray
                                                                    A47299
                                                                                                                              RESULT 43
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J. Biol. Chem. 260, 5328-5341, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated A;Reference number: A22248; MUID:85182674
A;Accession: A22248
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A;Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
R;Que, B.G.; Davie, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A00930; MUID:86033830 A;Accession: A00930
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J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of fa A;Reference number: A4466; MUID:92184750
A;Contents: annotation; carbohydrate binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Fujikawa, K.; McMullen, B.A.
J. Biol. Chem. 258, 10924 10933, 1983
A;Title: Amino acid sequence of human beta-factor XIIa.
A;Reference number: A21037; MUID:83291041
A;Accession: A21037
A;Accession: A21037
                                                                                                                                                                                                                                                                                                                                     F:217-295/Domain: kringle homology <kRG>
F:298-356/Region: proline-rich
F:298-356/Region: proline-rich
F:354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <8
F:354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <8
F:393-609/Domain: trypsin homology <TRY>
F:38-110,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-
F:308/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:308/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 5q34-5qter
A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 5
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anion
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A; Residues: 354-362; 373-615 <FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 146-378,'G',380-615 <QUE>
A;Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
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A;Accession: A25191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 25, 1525-1528, 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;47-88/Domain: fibronectin type II repeat homology <FB2>
F;98-130/Domain: EGF homology <EG1>
F;135-170/Domain: fibronectin type I repeat homology <IF1>
F;178-209/Domain: EGF homology <EG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: blood coagulation; fibrinolysis; glycoprotein; nydrolase; killigie; Plasma F;1-19/Domain: signal sequence #status predicted <SIG> F;20-372,373-615/Product; coagulation factor XIIa, alpha form #status experimental <A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolo C;Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB:F12
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                                                                                                                                                                                                                                                                                                            F;412,461,563/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Pathway: blood coagulation; fibrinolysis
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                                                                                                                                                      Matches
                                                                                                                                                                                                                       Query Match
267 RNPDNDI-RPWCFVLNRDRLSWEY 289
                                                                                                                                                      Local Similarity
les 10; Conserv
                                                                         1 RNPDGDVGGPWAYTTNPRKL-YDY 23
                                                                                                                                                      Conservative
                                                                                                                                                                                           35.5%;
41.7%;
                                                                                                                                                                                                                                       Score 49;
                                                                                                                                                                                               Pred. No. 34;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                       DB 1; Length 615;
                                                                                                                                                                      Gaps
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hypothetical protein MJ0145 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jan-2000
C:Accession: B64318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: 3
A:Introns: 17/3; 57/3; 90/3; 136/3; 183/1; 241/3; 310/3; 350/3; 390/3; 431/3; 466/3; 515
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
                                                                                                                                                                                                               B64318
                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;484-653/Domain: ATPase nucleotide-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein Sequence Database,
A;Reference number: Z25018
A;Accession: T49228
A;Status: preliminary
                                                                                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC clone F27H5 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasma membrane H+-ATPase-like - Arabidopsis thaliana
N;Alternate names: protein F27H5.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49228
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.: Rudd. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: ATSP: F27H5.120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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F;225,340,477,544/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L11311; NID:g290857; PIDN:AAA49285.1; PID:g290858
A;Experimental source: electric organ
A;Note: sequence extracted from NCBI backbone (NCBIN:128724, NCBIP:128726)
C;Superfamily: Torpedo ror-related receptor; immunoglobulin homology; kringle homology;
C;Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
E;44-103/Domain: immunoglobulin homology <IM)
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Proc. Natl. Acad. Sci. U.S.A. 90, 2895-2899, 1993
A;Title: Muscle-specific trk-related receptor with a kringle domain defines a distinct
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C:Species: Torpedo californica (Pacific electric ray)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
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A; Residues: 1-946 <JEN>
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57.1%;
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    Mismatches

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Pred. No. 6
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Pred. No. 54;
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                                                  A;Cross-references: EMBL:AF043693; PIDN:AAB97535.1; GSPDB:GN00019; CESP:C34B2.3
          A; Experimental source: strain Bristol N2; clone C34B2
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R;Graves, T.; Sutterer, C.; Hawkins, M.; Wilson, R. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid C34B2. A;Reference number: Z21241
A; Molecule type: DNA
A; Residues: 1-357 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Sammons, L.; WULLLINGER, December 1. Submitted to the EMBL Data Library, December 1. A. Description: The sequence of C. elegans cosmid F33D11.
                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                             A; Accession: T32881
                                                                                                                                                                                                          C; Accession: T32881
                                                                                                                                                                                                                        C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                       hypothetical protein C34B2.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans
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A:Introns: 34/3; 72/3; 104/2; 127/3; 159/3; 187/3; 260/3; 295/3; 324/3
C:Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                      T32881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F33D11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Coenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Reference number: A64300; MUID:96337999
A;Accession: B64318
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C; Superfamily: Methanobacterium conserved hypothetical protein MTH1017
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A; Residues: 1-268 <BUL>
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57.1%;
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196 NPDGDQGGP 204

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: F70662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ... Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable plcC protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: II C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC3603
2-oxolsovalerate dehydrogenase alpha chain (EC 1.2.4.4) [imported] - Brucella melitensi C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C;Accession: AC3603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:C34B2.3
A;Map position: 1
A;Map position: 1
A;Introns: 40/3; 79/3; 111/2; 134/3; 166/3; 194/3; 267/3; 302/3; 331/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                             A;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-508 <COL>
                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: F70662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: BMEII0748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE008918; PIDN:AAL53990.1; PID:g17984939; GSPDB:GN00191A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-410 < KUR>
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                                                                Query Match
Best Local
                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 NREGEAVGPWAGTLTDEELKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 PWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 6; Conserv
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  NPDGDVGGP 10
                                              Similarity
8; Conserv
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                                              Conservative
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42.9%;
                                                                34.8%;
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Pred. No. 30;
3; Mismatches
                                       Score 48; DB Pred. No. 38; 0; Mismatches
                                           0;
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26;
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                                                                                   Length 508;
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                                         Indels
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                                                                                                                                                                                          PIDN:CAB06146.1; PID:g1781256
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                                         0;
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                                       Gaps
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                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon,
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Search completed: November Job time: 17 secs
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                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans
                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07319.1; A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       н84099
                                                                                                                                                                                                                                                                                                               A; Residues: 1-461 <STO>
                                                                                                                                                                                                                                                                                                                                                                          A; Accession: H84099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 50
                                                                                                                                                                            Best
                                                                                                                                                                                            Query Match
                                                                                                                                                         Matches
                                                                           328 RPATGDISSPFGYRTHPVTGQRKLH 352
                                                                                                                                                       Local Similarity
les 10; Conserv
                                                                                                                1 RNPDGDVGGPWAYTTNP----RKLY 21
                                                                                                                                                                                                                                     BH3600
                                                                                                                                                         Conservative
                                                                                                                                                                        34.1%;
                  8,
                  2002,
                                                                                                                                                                        Score 47;
Pred. No.
                                                                                                                                                 Pred. No. 48;
4; Mismatches
                  09:32:03
                                                                                                                                                                      DB
48;
                                                                                                                                                                                            2;
                                                                                                                                                                                            Length 461;
                                                                                                                                                       Indels
                                                                                                                                                     4;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:31:21; Search time 26 Seconds (without alignments) 153.034 Million cell updates/sec

US-09-657-431-9

Title: Perfect score:

Sequence: 1 RNPDGDVGGPWAYTTNPRKLYDY 23

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database :

SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:* sp_fungi:*

3: 4: 5: 7: 7: 8: 9: 10: 113: 114: 115: 115: sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:* sp_mammal:*
sp_mhc:* sp_human:* sp_invertebrate:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	. ₩	ID	Description
ב	134	97.1	334	6	046507	046507 papio hamad
2	134	97.1	810	4	Q15146	Q15146 homo sapien
ω	128	92.8	812	11	Q91WJ5	Q91wj5 mus musculı
4	122	88.4	812	11	Q9R0W3	Q9r0w3 rattus norv
ហ	115	83.3	806	0	018783	018783 macropus eu
σ	94	68.1	716	11	P70521	P70521 rattus norv
7	90	65.2	709	13	Q90ZN6	Q90zn6 brachydanic
80	90	65.2	716	11	Q91XG8	Q91xg8 mus musculu
9	88	63.8	567	4	Q13208	Q13208 homo sapien
10	86	62.3	313	13	Q9PU78	Q9pu78 crocodylus
11	86	62.3	704	13	Q90865	Q90865 gallus gal
12	84	60.9	648	4	Q9H1V4	
13	81	58.7	728	6	Q9вн09	Q9bh09 felis silve
14	79	57.2	75	6	Q9BGN9	Q9bgn9 bos taurus
15	79	57.2	109	σ	Q9N1B8	Q9n1b8 ovis aries
16	79	57.2	208	4	Q9BYM0	Q9bym0 homo sapier

ALIGNMENTS

Дb

532 RNPDGDVGGPWCYTTNPRKLYDY 554

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Qy
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Q15146
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                              Matches
                                        Query Match
Best Local Similarity
                                                                                                                          SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50070; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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Q15146;
Q1504-1996 (Tremblrel. 01, C
01-NOV-1996 (Tremblrel. 01, L
01-DEC-2001 (Tremblrel. 19, L
PLASMINOGEN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                               PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 5.
                                                                                                                                                                                                                                                  InterPro: IPR001254; Trypsin.
Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00099; trypsin; 1.
                                                                              SEQUENCE
                                                                                                     SIGNAL
                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
Mitchell D., Robinson J.H.;
Mitchell D., Formhinant human plasminogen and aglycoplasminog
                                                                                                                                                                                                                                                                                                                                                       EMBL; M74220; AAA36451.1; -. HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                    InterPro; IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                        Fibrinolysis 0:0-0(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                           interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                .nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Serine protease.
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1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 RNPDGDVGGPWCYTTNPRKLYDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loca L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                     Serine protease; Signal.

1 19 POTENTIAL.
20 810 PLASMINOGEN.
                                                                                                                                                                                                                                                                                                                        IPR001314; Chymotrypsin. IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                 IPR003014; PAN.
                                                                             810 AA;
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AA; 36791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                          810 P:
; 90555 MW;
                                    97.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.18;
95.78;
                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                    Score 134; DB 4;
Pred. No. 3.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 134; DB 6;
Pred. No. 1.3e-11;
                                                                         B05C7D4B0D020B3C CRC64;
                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C7DC06E03B965286 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 AA.
                                                Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                        aglycoplasminogen
                        Indels
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                       0;
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                      Gaps
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RESULT 3
Q91WJ5
ID Q91W
AC Q91W
AC Q91W
DT 01-D
DT 01-D
DT 01-D
DT 01-D
CT 01-
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Best Local
                                                                                                                                                                                                                                                                                                                                        Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis autoantigen (GP330) as receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                     InterPro; IPR003609; Pan_app.
InterPro; IPR001400; SOMATOTR
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 5.
Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                               TRYPSIN FAMILY.

EMBL; AJ242649; CAB46014.1; -.

HSSP; P00747; 1PMK.
                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                         MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91WJ5;
Q91WJ5;
01-DEC-2001
                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bangert K.,
"Rat plasmir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R0W3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9R0W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 RNPDGDVNGPWCYTTNPRKLYDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen:
PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tted (OCT-2001) to the EMBL/GenBank/DDBJ databases BC014773; AAH14773.1; -. NCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                          IPR000001; Kringle. IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnsen A.H., Thorsen S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     BELONGS TO PEPTIDASE FAMILY S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA and gene structure.";
99) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114//3:1; -.
90781 MW; 24173260E6A2FFD2 CRC64;
                                                                                                         SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.8%;
91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 128; DB 11;
Pred. No. 2.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                     ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Query Match
Best Local Similarity
"-+-hes 18; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                      SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50040; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_ER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O18783;
O18783;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINCLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease; Signal. SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macropus eugenii (Tammar wallaby).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                     Pfam; PF00051; kringle; 5.
pfam; PF00024; PAN; 1.
pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00008; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMINOGEN.
                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin. InterPro; IPR000001; Kringle. InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                           EMBL; AF012297;
                                                                                                                                                                                                                                                                                                                                                                             "Convergent evolution of apolipoprotein(a) in primates and hedgehog."; Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
                                                                                                                                                                                                                                                                                                                                                                                                       Lawn R.M., Schwartz K., Patthy L.;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98004511; PubMed=9342350;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532
                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                   MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                        TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNPDGDVNGPWCYTMNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                  S01.233;
                                                                                                                                                                                                                                                    IPR003609; Pan_app.
IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 (TrEMBLrel. 05, 08 (TrEMBLrel. 05, 11) (TrEMBLrel. 19, 12)
                                                           Serine protease.
806 AA; 90981 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               5HPG.
                                                                                                                                                                                                                                                                                                                                           AAB65760.1;
                                                                                    TRYPSIN_DOM; 1.; TRYPSIN_HIS; 1.; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.4%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90535 MW;
                                                               90981 MW;
                        78.3%;
                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASMINOGEN
              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 122; DB 1:
Pred. No. 2e-09;
0; Mismatches
                          Score 115; DB 6; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8C703C51410EBC9E CRC64;
                                                               95FAA86DC20064D5 CRC64;
              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 812;
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                                    Length 806;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
              0;
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              Gaps
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RESULT
P70521
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Q90ZN6
ID Q0
AC Q0
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                                                                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                 В
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                   Q90ZN6 PRELIMINANA,
Q90ZN6;
Q90ZN6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HEPATOCYTE GROWTH FACTOR-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE STIMULATING PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00130; KR; 4.
SMART; SM00473; PAN AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P70521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P70521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X95096; CAA64473.1; HSSP; P00747; 1KRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 227:273-280(1996).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohshiro K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97011126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                      429 RNPDGDSHGPWCYTLDPETLFDY 451
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                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDPNGPWCYTTNPKKLFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00051;
PF00024;
                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IPR001314; Chymotrypsin.

; IPR000001; Kringle.

; IPR00304; PAN.

; IPR003609; Pan_app.

; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease; Signal.

1 31 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11126; PubMed=8858136; Iwama A., Matsuno K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kringle; 4.
PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%;
65.2%;
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                                                                                                                                                                                                                                                                                                                                                                                            ν,
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PÕTENTIAL.
; 06B7DF3EF56D921F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
    (Zebra danio)
Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ezaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                    2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakamoto
                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 716;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                           013208;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010551; AAH10551.1; -
SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;
                                                                                     SEQUENCE FROM N.A. MEDLINE-20191171; PubMed=10728827; Degen S.J.F., McDowell S.A., Waltz
                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           DNA Seq. 8:409-413(1998).
EMBL; U28054; AAC63092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                               Carritt B.;
                                                                                                                                                                                                                                                                     Q13208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                            "Structure of the human D1F15S1A locus: a chromosome 1 locus with
                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEPATOCYTE GROWTH FACTOR-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Early expression of zebrafish Hepatocyte Growth Factor-Like suggests a conserved role in vertebrate neural induction."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF370035; AAK54207.1; SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;
                                     like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91XG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                  dentity to the chromosome 3
                                                                                                                                                                                                                                                                                                                                       429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bassett D.I., Wilson S.W.; "Early expression of zebra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 RNPDGDHHGPWCYTSDPKTEFDY 444
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                                                                                                                                                                                                                                                                                                                                                            1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                    RNPDGDSHGPWCYTLDPDILFDY 451
P00747; 2PK4.
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.2%;
60.9%;
                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                              gene coding for hepatocyte growth factor-
                                                                                                                                                                                                                                                                                                                                                                                                              Score 90;
                                                                                          Waltz
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                      S.E., Gould F.,
                                                                                                                                                                                                                                                                  567 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 AA
                                                                                                                                                                                                                                                                                                                                                                                                  8.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 716;
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                                                                                        Stuart L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                             97%
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В
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                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00051; kringle; 4.
Pfam; PF00024; PAN; 1.
Pfam; PF000089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
                                                                                                             NON_TER
                                                                                                                                             SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                  SEQUENCE
                                                                                                                                                                                                         InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                          MEDLINE=20022983; PubMed=10555283; Hughes S., Zelus D., Mouchiroud D.; "Warm-blooded isochore structure in nile
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN (FRAGMENT).
Croccodylus niloticus (Nile croccodile) (African croccodile).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Croccodylidae; Croccodylinae; Croccodylus.
                                                                                                                                  Hydrolase; Serine protease
                                                                                                                                                                                                                                                                         Mol. Biol. Evol. 16:1521-1527(1999).
EMBL; AJ011396; CAB56422.1; -.
HSSP; P00747; 1HPJ.
                                                                                                                                                                                                                                                                                                                                                    TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PU78
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PU78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.977;
80 RNPDNDSHGPWCYTMDPRTPFDY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 QNPDGDSHGPWCYTMDPRTPFDY
                      1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                            Similarity
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                                                                                               313
313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease.
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                             313
                                                         62.3%;
60.9%;
                                                                                                34793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64117 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.8%;
60.9%;
                                               2;
                                                          Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88; DB 4;
Pred. No. 0.00013;
                                                                                               8E084704958B5AA2 CRC64;
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3FC38B07F1645810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AA
                                                          0.00013;
                                                                       DB 13;
                                                                                                                                                                                                                                                                                                            crocodile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6;
                                                                    Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 567
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                            turtle.";
                                             0;
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                                            Gaps
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Q9H1V4
ID Q9H1V
AC Q9H1V
AC Q9H1V
AC Q9H1V
AC JH1V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP; 1.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS00021; KRINGLE_2; 4.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90865

Q90865;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TREMBLREL 19, Last annotation update)
Q1-TYPE GROWTH FACTOR-LIKE/MACROPHAGE STIMULATING PROTEIN.
                                                                                                                                                                                                                                                                   O9H1V4 PRELIMINARY;
O9H1V4;
O1-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-DEC-2001 (TIEMBLIEL 1
DJ118ZA14.3 (SIMILIAR TO MORE)
GROWTH FACTOR-LIKE))).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96029010; PubMed=7554499;
Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
"Expression of HGF/SF, HGF/MSP and c-met suggests new functions during early chick development.";
Dev. Genet. 17:90-101(1995).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003011; PAN.
InterPro; IPR00309; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 4.
                    Bird C.;
Submitted (NOV-2000) to
-i- SIMILARITY: BELONGS
                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                   DJ1182A14.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00051; kringle; Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY
  TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNPDNDSHGPWCYTMDPRTPFDY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X84043; CAA58862.1; -. P00747; ICEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S01.977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease. 704 AA; 79341 MW; CABOD8CC41367C37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
                                                                                                                                                                                                                                                                                               16, 0
16, 1
19, 1
                       the EMBL/GenBank/DDBJ databases TO PEPTIDASE FAMILY S1; ALSO KN
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
1 (MACROPHAGE STIMULATING
                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.00031;
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                                                                                                                                                                                                                                                                                                                                                                                                                         A
                         KNOWN
                                                                                                                                                                                                                                                                                               1 (HEPATOCYTE
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                         AS
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                            THE
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A FOR THE PROPERTY OF THE PROP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                               InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 1.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00772; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                   Hydrolase;
SEQUENCE
                                                                                               SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; UNKNOWN_4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
Kobayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K.,
Tsujimoto H.;
Tsujimoto H.;
"Molecular cloning of feline hepatocyte growth factor (HGF) cDNA.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BH09;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS0070; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09вн09
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InterPro; IPR001254;
                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRY PRINTS; PR00018; KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY.
EMBL; AB046610; BAB21499.1; -.
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 RNPDGDPGGPWCHTTDP 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL137798; CAMPO0747; 5HPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00024; PAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 AA;
                                                   728 AA; 83067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease. 648 AA; 72781 MW; 4CE077057350E463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan_app.
     58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 84; DB 4;
Pred. No. 0.00056;
     Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                   8D7F4A333D1E190A CRC64;
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     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 648;
  Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis.
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Q9BGN9
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                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                      09N1B8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                     SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM FROM DAY 1 CYCL.
MEDLINE-20297031; PubMed-10819791;
Chen C., Spencer T.E., Bazer F.W.;
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0018; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN
SMART; SM00130; KR; 2.
PROSITE; PS00021; KRINGLE_1;
PROSITE; PS50070; KRINGLE_2;
                                                                                                          Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                         "Expression and action of hepatocyte growth factor in bovine endometrial stromal and epithelial cells in vitro."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB056447; BAB33031.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                             HEPATOCYTE GROWTH FACTOR (FRAGMENT).
                                                                                                                                                                             Q9N1B8
                                                                     NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P14210; 1BHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakami S., Fujiwara C., Miyamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
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    Expression of hepatocyte growth factor and its receptor c-met in the prine uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 RNPDDDAHGPWCYTGNPLIPWDY 461
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                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                           RNPRGEEGGPWCFTSNPEVRYE
                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                    75 AA;
                                                                                                                                   (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                Conservative
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54.5%;
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                                                                                                                                                                                                                                                                         Score 79;
Pred. No.
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1; Mismatches
                                                                                                                                                                                                                                                                                                   829EEEFCC49701B1 CRC64;
                                                                                                                                                                                                                                                                                                                                         UNKNOWN_1.
                                        CYCLIC UTERUS;
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                                                                                                                                                                                                                                                               6; Indels
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 Q13494
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 PRELIMINARY;
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SMART; SM00130; KR; 1.
SMART; SM00473; PAN_AP; 1.
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PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN
                                                                                                                                                                  PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                      InterPro; IPR003014;
InterPro; IPR003609;
InterPro; IPR003966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          human hepatocyte growth factor g
Biochemistry 30:9170-9176(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyazawa K., Kitamura A., Kitamura N.; "Structural organization and the transcription initiation site of the human hepatocyte growth factor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0018; KRINGLE.
SMART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=91369928; PubMed=1832556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Reprod. 62:1844-1850(2000).
EMBL; AF213397; AAF25945.1; -.
HSSP; P14210; 2HGF.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEPATOCYTE GROWTH FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50070; KRINGLE_2;
178 RNPRGEEGGPWCFTSNPEVRYE
                              1 RNPDGDVGGPWAYTTNPRKLYD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYD 22
                                                                                                                                                                                                                                                                                                                                                       M75971; AAG53459.1;
M75967; AAG53459.1;
M75966; AAG53459.1;
M75968; AAG53459.1;
M75969; AAG53459.1;
M75969; AAG53459.1;
P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNPRGEEGGPWCFTSNPEVRYE
                                                               l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
12; Conserv
                                                                                                                                   208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRINGLE_1;
                                                                                                                                                      208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                 57.2%;
54.5%;
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                                                                                                                                    23931 MW;
                                                                                                                                                                                                                                                                                                       PAN.
Pan_app.
                                                                                                                                                                                                                                                                                         Prothrombin
                                                                                                                                                                                                                                                                                                                                     Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                                                                                                                                                                                                                                                                                         JOINED
199
                                                               4;
                                                                               Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 79; DB 6;
Pred. No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                    AE9C50DE5A86B37B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1F88FE5DBC0D4A5D CRC64;
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                   0.00088;
                                                                                                 DB 4;
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                                                                 6;
                                                                                                 Length 208;
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                                                                 Indels
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PRT;

210 AA

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RESULT OF STATE OF ST
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Best Local
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O1-NOV-1996 (Tremblrel. (
O1-NOV-1996 (Tremblrel. (
O1-JUN-2001 (Tremblrel. J
HGF AGONIST/ANTAGONIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-JUN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       055027
055027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 1. SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00021; KRINGLE_1; 1. PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                Submitted (JAN-1998) to the EMBL; AF042856; AAC40051.1; HSSP; P14210; 1BHT.
                                                                                                                                                           "ISSUE-LUNG", May M., LaRochelle W.J.;

"""""++pd (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                  Jakubczak J.L., LaRochelle W.J., Merlino G.;
"NKI, a natural splice variant of hepatocyte growth factor/scatter
factor, is a partial agonist in vivo.";
Mol. Cell. Biol. 18:1275-1283(1998).
                                            MGD; MGI:96079; Hgf.
InterPro; IPR000001; Kringle
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98147766; PubMed-9488442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEPATOCYTE GROWTH FACTOR NK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNPRGEEGGPWCFTSNPEVRYE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U46010; AAC50539.1; -. P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                         IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.2%;
54.5%;
                         Pan_app
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
01,
17,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79; DB 4;
Pred. No. 0.00088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94A6EE9C50DE5A86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
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RESULT 19
Q02935
THE TET SEN DRAFT 
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update
01-JUN-2001 (TrEMBLrel. 17, Last annotation upda:
HEPATOCYTE GROWTH FACTOR, HEAVY CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
SEQUENCE 211 AA; 24308 MW; 758BD0687A835F48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q02935
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                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                 InterPro; IPR003609; Pan_app pfam; PF00051; kringle; 2. Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS TWO KRINGLE REGIONS.
-!- SIMILARITY: HIGH, TO OTHER HGF; LOWER, TO
EMBL; X57574; CAA40802.1; -.
EMBL; LO2931; AAA52649.1; -.
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An alternatively processed mRNA generated from growth factor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                              SMART; SM00130; KR; 2.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR0000001; Kringle
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93087571; PubMed=1280830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyazawa K., Kitamura A., Naka D., Kitamura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91200041; PubMed=1826653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                  SIGNAL
                                                                                                                                           Growth
                                                                                                                                                               PROSITE; PS00021; KRINGLE_1; 2. PROSITE; PS50070; KRINGLE_2; 2.
                                                                                                                                                                                                                                                        PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 RNPRGEEGGPWCFTSNPEVRYE 200
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                        32
128
211
32
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                                                                                                                                           Kringle;
                        290
206
288
32
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54.5%;
                                                                                                                                           Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79; DB 11;
Pred. No. 0.00089;
4; Mismatches 6
                        HEPATOCYTE GROWTH FACTOR, HEAVY
KRINGLE 1 (BY SIMILARITY).
KRINGLE 2 (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scatter factor/hepatocyte induces cell dissociation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO PLASMINOGEN
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TYPES. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 21
091691
ID 09169
AC 09169
AC 09169
AC 09169
DT 01-NC
DT 01-DE
DE GROWT
OS Xenoge
OC Eukar
OC Xenoge
OC Mumphi
OC Xenoge
OC MCBI_
RN (I)
RP SEQUE
RA SUJE
RA SUJE
RA SUJE
RA SUJE
RA SUJE
RA SUSDRI
DR HSSP;
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Q14519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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SEQUENCE FROM N.A.

Ruiz i Altaba A., Thery C.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases

EMBL; U57455; AAB52574.1; ~.

HSSP; P00747; 1CEA.
                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                      Q91691 PRELIMINARY; PRT; 716 AA.
Q91691;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
G1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GROWTH FACTOR LIVERTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q14519;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPETITIVE HGF ANTAGONIST.
                                                                                                                                                                     NCBI_TaxID=8355
                                                                                                                                                                                                   Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 2.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR00309; Pan_app.
Pfam; PF00051; Kringle; 2.
Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative Transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chan A.M.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P14210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 0:0-0(1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a Competitive HGF Antagonist Encoded by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aaronson S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q14519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 RNPRGEEGGPWCFTSNPEVRYE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNPDGDVGGPWAYTTNPRKLYD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPRGEEGGPWCFTSNPEVRYE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M77227; AAA35980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00021; KRINGLE_1; 2. PS50070; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 AA;
                                                                                                                                                                                              Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34546 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 4; Length 296; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A45E456B87AE03BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C8A18A6F0D63200A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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AC OCC CONTRACTOR OF THE CONTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                        InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003019; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 4.
Pfam; PF00024; PAN, 1.
Pfam; PF000089; trypsin; 1.
Pfam; PF00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00130; KR; 4.
SMART; SM00300; Trypsin; 1.
PROSITE; PS00021; KRINGLE_1; 3.
PROSITE; PS00021; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00130; KR; 4.

SMART; SM00473; PAN_AP; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                 SEQUENCE
                                                                                                             CHAIN
                                                                                                                       PROSIE; roserv, rosers, Signal, Hydrolase; Serine protease; Signal, errowar. 1 28 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrulation.";
mech. Dev. 54:23-37(1996).
EMBL; Y08734; CAA69989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The Xenopus homologue of hepatocyte growth factor-like specifically expressed in the presumptive neural plate d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aberger F., Schmidt G., Richter K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96404125; PubMed=8808403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P70006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00051; kringle; 4. Pfam; PF00024; PAN; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.UNA; -.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 RNPDRDSHGPWCYTMDPNTPFDY 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                               29
717 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease.
716 AA; 81971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1CEA.
                                                                               ΑA;
                                                                         717 H
; 82017 MW;
57.2%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.2%;
56.5%;
Score 79; DB 13;
Pred. No. 0.0034;
                                                                                                  HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 13;
Pred. No. 0.0034;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presumptive neural plate during
                                                                            6F877A432C8CDD54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508376A0E4398798 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717 AA
                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE: P800021; KRINGLE_1; 1.
PROSITE: P850070; KRINGLE_2; 1.
PROSITE: P850240; TRYPSIN_DOM; 1.
PROSITE: P800134; TRYPSIN_HIS; 1.
PROSITE: P800135; TRYPSIN_SER; 1.
                                                                                                 Q91402 PRELIMINARY;
Q91402;
01-NOV-1996 (TrEMBLrel. 01, 0
01-NOV-1996 (TrEMBLrel. 01, 1
01-DEC-2001 (TrEMBLrel. 19, 1
HEPATOCYTE GROWTH FACTOR.
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Q25101;
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Stolidobranchia; Pyuridae; Herdmania.
NCBI_TaxID-7733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; pF00051; kringle; 1.
pfam; pF00089; trypsin; 1.
pRINTS; pR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold J.M., Kennett C., Lavin M.F.; "Transient expression of a novel serine protease in the the ascidian Herdmania monus during development."; bev. Genes Evol. 206:455-463(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMSERP1
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000001; Kringle. InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.UPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Genes Evol. 206:455-463(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CURVATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
              Xenopodinae.
NCBI_TaxID=8353;
                                           Eukaryota; Metazoa; C
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Chymotrypsin.
                                                                       Xenopus
                                                                                                                                                                                                   24
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                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                            Serine protease.
385 AA; 42935 MW;
                                                        Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       TRYPSIN_DOM; 1.
TRYPSIN_HIS; 1.
TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                  56.5%;
                                            Anura; Mesobatrachia; Pipoidea; Pipidae;
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19,
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Last annotation updat
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                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                  Score 78; DB 5; Length 385; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                             BFB1D05D5232E6A0 CRC64;
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Q90978
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Best Local
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SMART; SM00473; PAN_BR; 1.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00021; KRINGLE_1; 3.

PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura H., Tashiro K., Nakamura T., Shiokawa "Molecular cloning of Xenopus HGF cDNA and its Xenopus early embryogenesis.";
Mech. Dev. 49:123-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prosite; ps50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
seQUENCE 710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S77422; AAB34354.2; -. HSSP; P14210; 1BHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95267690; PubMed=7748783;
                                                                                                                                                                                                                                                                                                                     HEPATOCYTE GROWTH FACTOR / SCATTER FACTOR PRECURSOR.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q90978
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                                                                                                                                                                           MEDLINE-96029010; PubMed-7554499; Thery C., Sharpe M.J., Batley S.J., S "Expression of HGF/SF, HGFI/MSP, and during early chick development."; pev. Genet. 17:90-101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                        Q90978; Q90866;
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                    node during gastrulation.";
Development 121:813-824(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
                                                              Streit A., Stern C.D., Thery C., Ireland G.W., Sharpe M.J., Gherardi E.; "A role for HGF/SF in neural induction and its
                                                                                                                       TISSUE-EMBRYO;
                                                                                                                                   STRAIN=WHITE LEGHORN, AND RHODE ISLAND RED X LIGHT
                                                                                                                                                  SEQUENCE OF 1-409 FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                        MEDLINE=95237013; PubMed=7720585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 RNPDNDAHGPWCYTDDPFVPWDY 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKLYDY 23
          TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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IPR003609; Pan_app
IPR001254; Trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001314; Chymotrypsin.
IPR000001; Kringle.
IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kringle; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%;
56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78;
Pred. No.
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                                                                                              Ireland G.W.,
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                                                                                                                                                                                                            c-met suggests
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                                                                   expression in Hensen's
                                                                                            Aparicio
                          ALSO KNOWN AS THE
                                                                                                                                                                                                                          Gherardi E.;
                                                                                                                                         SUSSEX;
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Q28398
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                                                Query Match
Best Local :
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Best Local :
                                                                                                                                                                 InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 31.
                                                                                                                                                                                                                                                                                                                              Erinaceus europaeus (Western European hedgehog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinac
                                                                                   SEQUENCE
                                                                                                NON_TER
                                                                                                                    PROSITE; PS00021; KRINGLE_1; 17. PROSITE; PS50070; KRINGLE_2; 31.
                                                                                                                                            PRINTS; PRO0018; KRINGLE. SMART; SM00130; KR; 31.
                                                                                                                                                                                          #Hedgehog apolipoprotein(a).";
J. Biol. Chem. 270:24004-24009(1995).
EMBL; U33170; AAC48522.1;
HSSP; P00747; 1PMK.
                                                                                                                                                                                                                                 Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P., Byrne C.D., Fong K.J., Meer K., Patthy L.; "The recurring evolution of lipoprotein(a). Insights from cloning
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
APOLIPOPROTEIN(A) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q28398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                          MEDLINE=96025778; PubMed=7592597;
                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9365;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q28398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing; Glycoprotein; Growth factor; Hydrolase; Kringle; Serine protease; Serine protease homolog; Signal.

1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                           ipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
          1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RNPDGDVGGPWAYTTNPRKLYDY 23
 RNPDDDFHGPWCYTDDPLIPWDY 461
                                    13; Conserv
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X80131;
P14210;
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PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00051; kringle; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                   2869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001254; Trypsin.
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IPR003609;
                                   Conservative
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82913 MW;
                                           56.5%;
                                                                                318601 MW;
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56.5%;
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                                Pred. No. 0.14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                        Score 72.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 13;
Pred. No. 0.0094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                              9527CEF985A4FB2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             2869 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 726;
                                                        DB 6;
                                6;
                                                       Length 2869;
                                Indels
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                                                                                                                                                                                                                                                                                                                                 Erinaceus.
                                1:
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                                Gaps
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RESULT 28
Q16609
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042341
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01-NOV-1996
01-JUN-2001
                              a single kringle domain.";
Arterioscler Thromb. Vasc. Biol. 15:65-70(1995).
EMBL; U19518; AAA85693.1;
EMBL; U19517; AAA85692.1;
EMBL; P00747; IPMK.
                                                                              Pfam; PF00051; kringle; 1
                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       042341 PRELIMINARY;
042341; O1-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                         MEDLINE=95268939; PubMed=7749817;
                                                                                                                                                                                                                     APOARGC
                                                                                                                                                                                                                                                                            Q16609;
                                                                                                                                                                                                                                                                                      Q16609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The expression of hepatocyte growth factor mRNA is temporally relevant to cardiac endothelial-mesenchymal transformation."; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. EMBL; D63779; BAA33643.1; -. HSSP; P00747; IKRN.
                    InterPro; IPR000001; Kringle
                                                                                                                                      TISSUE-LIVER;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                              (APOARGC).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00130; KR; 2.
PROSITE; PS00021; KRINGLE_1;
PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                           198 RNPDDDSHGPWCYTDDP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGF ALPHA-CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2548 RNPDGEV-APWCYTTNSAMRWEY 2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isokawa K., Yahagi N., Honma J., Tanaka M., Murakami K., Yokoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                  1 RNPDGDVGGPWAYTTNP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00051; kringle; 3.
S; PR00018; KRINGLE.
PR00018; KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     215
215 AA;
                                                                                                                                                                                                                                                              (TrEMBLrel.
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; 24949 MW;
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64.7%;
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Pred. No. 0.037;
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RESULT
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Best Local S
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proSITE; PS00021; KRINGLE_1; 1.
proSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TREMBLrel. 19, Created)
01-DEC-2001 (TREMBLrel. 19, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
PUTATIVE THROMBIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lepidosauria; Squamata; Sclerog
Colubridae; Colubrinae; Elaphe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90WS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90WS2
                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes S., Laurin M., Gouy M., Mouchiroud D.;
"The phylogenetic position of turtles among sauropsidae remains contentious with new nuclear data.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elaphe sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THROMBIN
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                              046506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=114965;
                                                                                 Cox L.A., Jett C., Hixson J.E.;
"Molecular Basis of the Applipoprotein (a) Null Phenotype:
Site Mutation is Associated with Deletion of a Single Exon
                                                                                                                                                                                Cercopithecinae; Papio
                                                                                                                                                                                                                                                  BABAPOA.
                                                                                                                                                                                                                                                                 APOLIPOPROTEIN A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                               046506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=9557;
                                                                                                                                                                                                                                 Papio hamadryas (Hamadryas baboon).
                                Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                   Allele.'
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
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                    TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ286868; CAC69543.1; -.
   AF029691; AAB97886.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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47.8%;
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Pred. No. 0.
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Q91001
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SMART; SM00020; Tryp_SPc; 1.

SMORT; SM00020; Tryp_SPc; 1.

PROSITE; PS000021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
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Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of through the characteristic of the B chain of through the characteristic of the B chain of through the characteristic of the chara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                     Banfield D.K.;
Submitted (DEC-1991) to the EMBL; M81391; AAA21619.1;
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                               encoding chicken and hagfish prothrombin."; J. Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-94223694; PubMed-7513365;
Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
"Evolution of prothrombin: isolation and characterization of the cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 RNPDADT-GPWCFTMDPSVRWEY 173
                                                                                                                                                                                                                                                                                                         TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                        InterPro; IPR001254; Trypsin.
InterPro; IPR000294; VitK_dep_GLA
                                                                                                                                                                            MEROPS; S01.217
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PF00594; gla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 AA; 50041 MW;
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                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
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19,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              974E30744C187B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 0.27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1:
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ACCOCK RRAC OCCOCK DD DR RRAC 
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Q9PTW7
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SMART; SM00130; KR; 2.

SMART; SM00120; Tryp_Spc; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS500134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002001; Kringle.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; VitK_dep_GLA.
Pfam; PF00594; gla; 1
Pfam; PF00594; gla; 1
Pfam; PF00595; kringle; 2.
Pfam; PF00051; kringle; 2.
Pfam; PF00001; GLABLOOD.
PRINTS; PR00010; GLABLOOD.
PRINTS; PR00011; GLABLOOD.
PRINTS; PR00011; GLABLOOD.
PRINTS; PR00011; GLABLOOD.
PRINTS; PR00011; GLABLOOD.
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Best Local :
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PRINTS; PRO0001; GLABLOOD.

PRINTS; PRO00018; KRINGLE.

PRINTS; PRO00018; KRINGLE.

PRINTS; PRO00130; KR; 2.

SMART; SM000130; KR; 2.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB028871; BAA89046.1; -. HSSP; P00734; luvs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Int. J. Biochem. Cell Blul. 32.1131 1137.2007.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20579470; PubMed=11137455; Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa Prost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa Purification and characterization of ostrich prothrombin."; Int. J. Biochem. Cell Biol. 32:1151-1159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Struthio camelus (Ostrich).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PTW7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8801;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 RNPDNNSEGPWCYTRDP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00089; trypšin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00051; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S01.217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease. 607 AA; 69110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.4%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           002F3606EA36270F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Q90WP0
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Best Local
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                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  TISSUE=LIVER;
Hughes S., La
                          SEQUENCE FROM N.A.
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys
                                                                                       Trachemys scripta elegans.
                                                  NCBI_TaxID=31138;
                                                                                                       THROMBIN.
                                                                                                               PUTATIVE THROMBIN (FRAGMENT).
                                                                                                                                                                     Q90WP0;
                                                                                                                                                                               090WP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=21181705; PubMed=11285247;

Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;

"Single nucleotide polymorphisms in exons of the apo(a) kringles types 6 to 10 domain affect Lp(a) plasma concentrations and have
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00747; 1PMK.
InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   different patterns in Africans and Caucasians.";
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Mol. Genet. 10:815-824(2001).
EMBL; AF158663; AAF03680.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOA.
Homo sapiens (Human).
Homosapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                           61 RNPDADT-GPWCFTMDPSIRWEY 82
                                                                                                                                                                                                                                                                  1 RNPDGDVGGPWAYTTNPRKLYDY 23
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                                                                                                                                                                                                                                                                                                       Similarity
  Laurin
                                                                                                                                                                                                                                                                                                                                              113 AA;
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                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                             Conservative
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 Ϊ.
                                                                                                                                                                                                                                                                                                                                                          113
                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                            12685 MW;
                                                                                                                                                                                                                                                                                                       46.0%;
Gouy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.4%;
58.8%;
                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                      Score 63.5; DB 4; Pred. No. 0.083;
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                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                           F3D65681D9B5253A CRC64;
Mouchiroud D.;
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                                                                                                                                                                                                                                                                                           Indels
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RESULT
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ID 077688
O77688
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O77688
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DT 01
DT 01
DT 01
DT 01
DT 01
OC ECC
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Best Local S
Matches 10
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Best Local :
                                                       077688;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                    PROTHROMBIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UIR8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The phylogenetic position of turtles among sauropsidae remains contentious with new nuclear data."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ286869; CAC69549.1; -.
                                                                                                       077688
                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000001; Kringle.
Pfam; PF00051; Kringle; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Hum. Mol. Genet. 10:815-824(2001).
EMBL; AF158656; AAF03677.1; -
EMBL; AF158655; AAF03677.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                           "Single nucleotide polymorphisms in exons of the apo(a) kringles types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21181705; PubMed=11285247;
Ogorelkova M., Kraft H.G., Ehnholm C.,
"Single nucleotide polymorphisms in exc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APOLIPOPROTEIN(A) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UIR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
           Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                               Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35
                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                 RNPDAEI-SPWCYTMDPNVRWEY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDDDDEGVWCYVDHPNTTFEY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                  P00747; 2PK4.
                                                                                                                                                                                                                                                                                                           PS50070;
                                                                                                                                                                                                                                                                                                                        PS00021;
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378 AA;
                                                                                                                                                                                                                                                             105 AA;
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105
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                                                                                                       PRELIMINARY;
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                          KRINGLE_1;
KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378
                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                             11882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42817 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.7%;
                                                                                                                                                                                                                         45.3%;
                                                      08, Created)
08, Last sequence update)
19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63;
Pred. No.
                                                                                                                                                                                      23
                                                                                                                                                                                                                         Score 62.5;
Pred. No. 0
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                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                             6ECB6C02CD30EFA2 CRC64;
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                                                                                                                                                                                                              Mismatches
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                                                                                                       Ā
                                                                                                                                                                                                                                    DB 4;
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           Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                    Length 105;
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RESULT 37
Q13209
ID Q1320
AC Q1320
DT Q1-NC
DT Q
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Best Loc
Matches
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Best Local
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                            PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q13209
Q13209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NEW ZEALAND WHITE; TISSUE-LIVER;
MEDLINE-99003227; PubMed-9786880;
Lee T.H., Rhim T., Kim S.S.;
"Prothrombin kringle-2 domain has a growth inhibitory activity against
                                                                                                                   Hydrolase;
NON_TER
                                                                                                                                                                                                                                                                                Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; U28055; AAC35412.1; HSSP; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Seq. 8:409-413(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carritt B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20191171; PubMed=10728827;
Degen S.J.F., McDowell S.A., Waltz S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF080065; AAC71006.1; HSSP; P00735; 1A0H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the human D1F15S1A locus: a chromosome 1 locus with 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              like protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identity to the chromosome
                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNPDGDEEGAWRYVAGRPSSFEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibroblast growth factor-stimulated capillary endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PR00018; KRIN
SM00130; KR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 273:28805-28812(1998).
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111 AA;
                                                                                                                                      Serine protease.
                                                                                             286 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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12168 MW; CB86624D8D7F9DE9 CRC64;
                                                                                             31986 MW;
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                      43.5%;
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                      Score 60; DB 4
Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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Pred. No. 0.27;
                                                                                             43489B747C8D3F90 CRC64;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286
                                              DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    s1;
                                            Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSO KNOWN AS
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor-
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GPWAYTTNPRKLYDY

23

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RESULT
Q9UIR7
ID Q9
AC Q9
AC Q9
DT 00
DT 00
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DT 00
AC Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                   "Single nucleotide polymorphisms in exons of the apo(a) kringles types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians."; Hum. Mol. Genet. 10:815-824(2001).
                                                     HSSP;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21181705; PubMed-11285247;
Ogorelkova M., Kraft H.G., Ehnholm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21181705; PubMed=11285247;
MEDLINE=21181705; PubMed=11285247;
Ogoralkova M., Kraft H.G., Ehnholm C., Utermann G.;
"Single nucleotide polymorphisms in exons of the apo(a) kringles
"Single nucleotide polymorphisms in exons of the apo(a) kringles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APOLIPOPROTEIN(A) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UIR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UIR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00747; 1KRN.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          types 6 to 10 domain affect Lp(a) plasma concentrations and different patterns in Africans and Caucasians.";
Hum. Mol. Genet. 10:815-824(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UKJ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00130; KR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APOA.
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                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDAEI-RPWCYTMDPSVRWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPWCYTMDPRTPFDY 17
                                                  AF158659; AAF03678.1; -. AF158658; AAF03678.1; JOINED. P00747; 2PK4.
     PF00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF158657; AAF03676.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
10; Conserv
                         IPR000001; Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O (TrEMBLrel.
O (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                   ; Chordata;
; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13, Created)13, Last sequence update)19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ν</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5719AA26B3E0FF1D CRC64;
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
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Q90504
  밁
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Best Local
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NON_TER
NON_TER 1
Hydrolase;
SEQUENCE
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Q90504;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81393; AAA21620.1; -. HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLIEGL. 01, 01-NOV-1996 (TREMBLIEGL. 01, 01-DEC-2001 (TREMBLIEGL. 19,
                                             PROSITE; PS00134; PROSITE; PS00135;
                                                                                                                                                                                                 SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banfield D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nine different species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissue=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                           PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Serine
420 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
protease.
; 47888 MW;
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SQ
                                                                               SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                       InterPro; IPR001254; Trypsin. Pfam; PF00051; kringle; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eptatretus stoutii (Pacific hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Evolution of prothrombin: isolation and characterization encoding chicken and hagfish prothrombin."; J. Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92212913; PubMed=1557383;
Banfield D.K., MacGillivray R.T.;
Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00018; KRINGLE SMART; SM00130; KR; 1.
                                                                                                                                                                                                                     PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                      InterPro; IPR001314; Chymotry
InterPro; IPR000001; Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94223694; PubMed=7513365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RNPDAEI-RPWCYTMDPSVRWEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad. Sci. U.S.A. 89:2779-2783(1992)
                                      TRYPSIN_HIS; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                             Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                       TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
64522AA21A57B67A CRC64;
                                                             UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4F80ADF8708548CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the cDNAs
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RESULT 42
Q96FE7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                Query Match
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Best Local Similarity
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000318;
01-JUL-1997 (TrEMBLrel. 0.
01-JUL-1997 (TrEMBLrel. 0.
01-DEC-2001 (TrEMBLrel. 1.
WUGSC:DJ515N1.2 PROTEIN.
WUGSC:DJ515N1.2.
                                                                                                                                                             Q96FE7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:17330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC002073; AAB54054.1; HSSP; P00749; 1KDU.
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00051; kringle; 1. PRINTS; PR00018; KRINGLE; SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
SEQUENCE 263 AA; 28248 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000318
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       Q96FE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Du Z., Scheet P., Harper M.; "The sequence of H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                           Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; BC011049; AAH11049.1; -
                                                                              SEQUENCE FROM N.A.
TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                  SEQUENCE
                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000001; Kringle.
                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                71 RNPDEDPRGPWCYVS
                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                      1 RNPDGDVGGPWAYTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNPDGDSEGVWCYT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNPDGDVGGPWAYT
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                                                                                                                                                                                                                                                                                                                            ! Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ence of H. sapiens PAC clone RP3-515N1."; (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                  263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       KRINGLE; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.8%;
                                28234 MW;
                                                                                                                                                                                                                                                                                                                                        40.6%;
                                                                                                                                                                                                                                                                                 85
40.6%;
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04,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; L
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                        Score 56;
Pred. No.
Score 56; DB 4; Pred. No. 2.6;
                                                                                                                                                                                                                         PRT;
                                   197C3EEE888FA242 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           197C3EEE8E54A242 CRC64;
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1.6;
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                                                         databases
                                                                                                                                                                                                                                                                                                                                                   Length 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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RESULT 44
Q9UIR6
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                                                                          STINDERS OF THE CONTRACT OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                    Query Match
Best Local Similarity
                                                                                             Lipoprotein.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC011256; AAH11256.1; -. SEQUENCE 559 AA; 63122 MW; 8CCEE2BDB94514D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
SIMILAR TO PLASMINOGEN ACTIVATOR, TISSUE.
                                                                                                                                                                                                                                                                                                                 "Single nucleotide polymorphisms in exons of the apo(a) kringles types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";

Hum. Mol. Genet. 10:815-824 (2001).

EMBL; AF158661; AAF03679.1; ...

EMBL; AF158660; AAF03679.1; JOINED.

HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91VP2;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UIR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91VP2
                                                                                                                                                                                                                                             InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 1.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21181705; PubMed=11285247;
Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APOLIPOPROTEIN(A) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UIR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOA.
                                                                     SEQUENCE
                                                                                                                                                                        PROSITE;
                                                                                                                                                                                               PROSITE; PS00021;
                                                                                                                                                                                                                           SMART; SM00130; KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 RNPDGD-ARPWCHVMKDRKLTWEY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNPDGDVGGPWAYTTNPRKL-YDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPDEDPRGPWCYVS
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                                                                                                                                                                          PS50070;
                                                                        113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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113
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                                                                                                                                                                        KRINGLE_1;
KRINGLE_2;
                                                                        113
12697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.6%;
  40.2%;
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Pred. No. 5.
  Score
Pred.
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                                                                          51D4461D9C66312E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
  . No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Matches

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RESULT
Q9UGS5
        Matches
                                Query Match
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Best Local
                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK747E2.4 (NOVEL KRINGLE AND CUB DOMAIN PROTEIN) (FRAGMENT).
                                                          SEQUENCE
                                                                       NON_TER
                                                                                            PROSITE; PS00021; KRINGLE_1; 1. PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                       PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 1.
                                                                                                                                  PRINTS;
                                                                                                                                                 Pfam; PF00051; kringle;
                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; ALO21393; CAB62959.1; -. HSSP; P00747; LPML.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         BK57G9.1
                                                                                                                                                                                                                                                                                                                                                                         Q9UGS5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                        Q9UGS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hughes S., Laurin M., Gouy M., Mouchiroud D., "The phylogenetic position of turtles among sauropsidae contentious with new nuclear data."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crocodylus niloticus (Nile crocodile) (African crocodile).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Crocodylinae; Crocodylus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                  SOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90WT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8501;
                                                                                                                                                                                                                                                                                                                                                                                                               46
                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPDGDEEGVWCVTQGEPDNFEY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ286873; CAC69536.1; -.
        10;
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                       117
117 AA;
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382
.; 43282 MW;
                                                      12673 MW;
                39.5%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.9%;
    Score 54.5; DI
Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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••
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                       F4270BBA1D03EDCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FE8E60239D8CBECB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 382;
5.5;
                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sauropsidae remains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
    2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                           Length 117;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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    1;
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    Gaps
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  RESULT 47
Q90Y90
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 48
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                               InterPro; IPR000859; CUB.
InterPro; IPR000001; Kringle.
InterPro; IPR002889; WSC.
Pfam; PF00431; CUB; 1.
Pfam; PF01822; WSC; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00042; CUB; 1.
SMART; SM00130; KR; 1.
SMART; SM00321; WSC; 1.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21167372; PubMed=11267660;
Nakamura T., Acki S., Kitajima K.,
                                                                                                                              EMBL;
                                                                                                                                          Biochim. Biophys. Acta
                                                                                                                                                     containing transmembrane protein.";
Biochim. Biophys. Acta 1518:63-72(2001).
                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.
                                                                                                                    HSSP;
                                                                                                                                                                                "Molecular cloning and characterization
                                                                                                                                                                                              Matsumoto K., Nakamura T.;
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                               Q9BY70;
                                                                                                                                                                                                                                                                                                                                                                                             Q9BY70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of containing transmembrane protein."; Biochim. Biophys. Acta 1518:63-72(2001). EMBL; AB070851; BAB64294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-21167372; PubMed-11267660;
Nakamura T., Aoki S., Kitajima K.,
Matsumoto K., Nakamura T.;
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Pfam; PF00051; kringle; 1.

Pfam; PF01022; WSC; 1.

PRINTS; PR00018; KRINGLE.

SMART; SM00042; CUB; 1.

SMART; SM00130; KR; 1.

SMART; SM00321; WSC; 1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.

PROSITE; PS500070; KRINGLE_2; 1.
                      Q924S4;
01-DEC-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.
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KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.
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-i- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB059617; BAB40968.1; -.
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InterPro; IPR000001; Kringle.
InterPro; IPR002889; WSC.
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time :
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21167372; pubMed-11267660;
Nakamura T., Aoki S., Kitajima K.,
Nakamura T.;
                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                       SEQUENCE
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Pred. No. 8
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:31:20; Search time 10 Seconds (without alignments) 89.055 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-657-431-9 138 1 RNPDGDVGGPWAYTTNPRKLYDY 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

105224

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32.6	33.0	33.0	33.0	33.0	33.3	33.3	33.3	33.3	33.7	34.1	34.8	34.8	35.1	35.5	36.6	37.0
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ALIGNMENTS

RL RP RL	RT RAX	RA R				RESULT PLMN_H ID P AC P DT 2
Eur. J. Biochem. 5 [6] SEQUENCE OF 95-580 SOTTRUP-Jensen L., (In) Davidson J.F. Progress in chemic	SEQUENCE OF 20-100. MEDLINE-75093329; Pub Wiman B. Wallen P.; "Structural relations of human plasminogen activation peptide as	Sottrup-Gensen L., Pe Soubmitted (JUL-1977) [4] SEQUENCE OF 292-810 J MEDLINE-85023311; Pul Malinowski D.P., Sadd "Characterization of human and bovine plan Biochemistry 23:4243	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-87162490; Forsgren M., Rader "Molecular cloning for human plasming for human plasming FEBS Lett. 213:254	SEQUENCE FROM MEDLINE-902028 Petersen T.E., "Characterizat in the fibrino J. Biol. Chem.	16-OCT-2001 (Rel. 40, Plasminogen precursor PLG. Homo sapiens (Human). Eukaryota; Metazoa; C Mammalia; Eutheria; P MCBI_TaxID=9806;	T 1 HUMAN PLMM_HUMAN PO0747; 21-JUL-1986 01-MAR-1989
Biochem. 50:489-494(1975) OF 95-580; 581-626; 657- Jensen L., Claeys H., Zaj idson J.F., Rowan R.M., S in chemical fibrinolysis	PubMed- P:; p:; ionship gen and e as stu	tc tc frc bMe bMe a a a	MEDLINE-87162490; PubMed=3030813; MEDLINE-87162490; PubMed=3030813; Forsgren M., Raden B., Israelsson M., L. "Molecular cloning and characterization "molecular cloning and characterization for human plasminogen."; FEBS Lett. 213:254-260(1987). [3]	MEDLINE-90202879; PubMed-2318848; Petersen T.E., Martzen M.R., Ichino Petersen T.E., of the gene for h "Characterization of the gene for h in the fibrinolytic system."; J. Biol. Chem. 265:6104-6111(1990).	ਜੇੜਾ	STANDARD; (Rel. 01, Created)
94(1975). 26; 657-700 AND H., Zajdel M., R.M., Samama M	-122932; between 'glutamic their interaction ddied by affinity'	E., R da R da Davi Davi	0813; lsson M., cterizati	3848; Ichinose A e for human ; (1990).	annotation update 3.4.21.7) [Contain 3.4.21.7] [Contain graph of the state of the s	PRT;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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MEDLINE=91095410; PubMed=1986355;
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MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE. SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRANSLEY MEASURED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3101. Chem. 264:5957-5965(1989).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND YON WILLEBRAND FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                         J04697; AAA36901.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212:541-552(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%;
95.7%;
                                                   Chymotrypsin.
                              Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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No. 1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence, evolution, and sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 810 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito H., Shinmyozu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 810;
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QY
                              Matches
                                            Query Match
Best Local
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SMART; SM00070; Tryp_SPC; 1.

PROSITE: PS00071; KRINGLE_1; 5.

PROSITE: PS50070; KRINGLE_2; 5.

PROSITE: PS50240; TRYPSIN_BOM; 1.

PROSITE: PS00134; TRYPSIN_HIS; 1.

PROSITE: PS00135; TRYPSIN_SER; 1.
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ACT_SITE
ACT_SITE
BINDING
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DOMAIN
DOMAIN
                                                                                                 DISULFID CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00722; CHYMOTRY PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00024; PAN; 1. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003609; InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00051; kringle;
                                                                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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 1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     remodeling;
                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease; Plasma; Glycoprotein; Fibrinolysis; odeling; Blood coagulation; Kringle; Zymogen; Signal.
                                                                                     810
                                                                                                                                                                                                                                                                                                                49
53
103
124
152
185
188
206
234
                              Conservative
                                                                                     AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPSIN_HIS; 1. TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                    335514661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypsin.
                                                                                     90255
                                         94.2%;
91.3%;
                                                                                      MW;
                                                                                  FIBRIN.

BY SIMILARITY.

BY SI
                             1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRINGLE
KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
  23
                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMEGA-AMINOCARBOXYLIC
OMEGA-AMINOCARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMEGA-AMINOCARBOXYLIC OMEGA-AMINOCARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRINGLE 5.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASMIN HEAVY CHAIR
ACTIVATION PEPTIDE
PLASMIN SHORT FORM
                                                         Score 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMEGA-AMINOCARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMINOGEN
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGHT CHAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAVY CHAIN
                                             4e-11;
                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORM OF CHAIN A.
                                                       Length 810;
                                                                                                  .) (BY SIMILARITY).
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACIDS.
ACIDS.
ACIDS.
ACIDS.
                              0,
                                Gaps
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В

RNPDGDVGGPWCYTTNPRKLFDY

0

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PLMN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P20918;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Plasminogen precursor (EC 3.4.21.7) [Contains:
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
InterPro; IPR003609; Pan_app
InterPro; IPR001254; Trypsin
Pfam; PF00051; kringle; 5.
                                                        MEROPS; S01.233; -.
MGD; MGI:97620; P1g.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
"Anglostatin: a novel anglogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma.";
Cell 79:315-328(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91184812; PubMed=2081600;
Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.
"Characterization of the cDNA coding for mouse pla
localization of the gene to mouse chromosome 17.";
Genomics 8:49-61(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE MEDLINE=95042728: PubMed=7525077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLMN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATORS, BOTH PLASMINGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANGOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN INMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANGOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELL TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

SIMILARITY: CONTAINS 5 KRINGLE DOMÁINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTECUTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMERYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAFIAN FOLLICLE. IT ACTIVATES THE URCKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LANING NAME OF AN ACTICALIST.
                                                                                                                                                                                 38514; A38514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND METASTATIC TUMORS IN VIVO.
ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
                                                                                                                                                              P00747;
                                                                                                                                                                1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for mouse plasminogen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elliott R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae; Mus
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15-DEC-1998 16-OCT-2001

(Rel. 37, Created)
(Rel. 37, Last sequence up
(Rel. 40, Last annotation
(EC 3.4.21.7) (Fragment).

update)

P81286; 15-DEC-1998

PLMN_SHEEP

STANDARD;

343 AA

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PLMN_SHEEP
        RESULT
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                                                                                           Matches
                                                                     Query Match
Best Local
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DISULFID
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DISULFID
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                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                     DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM;
                               532
                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00130; KR; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRY PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                              1 RNPDGDVGGPWAYTTNPRKLYDY
                              RNPDGDVNGPWCYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                              remodeling;
                                                                    Similarity
                                                                                                                 Serine protease; Plasma; Glycoprotein; Fibrinolysis;
                                                             Conservative
                                                                                          AA;
                                                                                        449
5560
5543
555
586
625
625
768
748
786
9084
                                                                                                                                                                             19
812
581
                                                                                                                                                                                                                                                                                                                                                                                                               Blood coagulation; Kringle;
                                                                    92.8%;
91.3%;
                                                                                           WW;
                                                            0;
                                                                                                  CHARGE RELAY SY.
CHARGE RELAY SY.
EY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                  ANGIOSTATIN.

PLASMIN LICHT CHAIN B.

KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

KRINGLE 5.
                                              23
                                                                    Score 128; DB 1; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                     SERINE
CHARGE
                                                                                                                                                                                                                                                                                                                                                                                ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                         PLASMIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                          PLASMIN SHORT FORM OF CHAIN
                                                                                          D34A74A4FC2256F8 CRC64;
                                                            Mismatches
                                                                                                                                                                                                                                                                                     E PROTEASE.

RELAY SYSTEM

RELAY SYSTEM
                                                                                                                                SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                               Zymogen;
                                                                           Length 812;
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(BY
                                                                                                                                                                                                                                                                                     Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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                                                            Gaps
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SOLUTION OF STREET STRE
PLMN_ERIEU
ID PLMN_E
AC Q2948_E
AC Q2948_D
DT 01-NOV
DT 01-NOV
DT 16-OCT
DE Plasmi
GN PLG.
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LI PROTEIN SEG. Data Anal. 5:21-25(1992).

LI PROTEIN SEG. Data Anal. 5:21-25(1992).

C -!- FUNCTION: DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS THE FUNCTION. IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYCONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, C AMD INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLACENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH ACTIVATOR, COLLACENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMEOSPONDIN, C LAMININ AND VON WILLEBRAND FACTOR.

C AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMEOSPONDIN, C LAMININ AND VON WILLEBRAND FACTOR.

C -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

C -!- SIMPLE ACTIVATED WITH STREPTOKINASE.

-!- SIMPLE ACTIVATED WITH STREPTOKINASE.

-!- SIMPLE ACTIVATES FOR DESCRIPTION FROM THE CLOTARIES ACTIVATED WITH STREPTOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93149995; PubMed=1492092;
Schaller J., Straub C., Kampfer U., Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis aries (Sheep).
                                                                                                                            PLMN_ER
Q29485;
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Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000001;
InterPro; IPR001254;
                                                  01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.233
                          Plasminogen
                                                                                                       01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                 66 RNPDGDVNGPWCYTTNPRKLFDY 88
                                                                                                                                                                                                                                                                                                                                 1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY. SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS.
                                                                                                                                                          ERIEU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1
141
<1
41
114
114
1181
1224
319
343
343
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                                                  (Rel.
(Rel.
(Rel.
                          precursor
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                       STANDARD;
                                             35,
40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood coagulation; Kringle; Zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
341
181
224
319
343
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Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           89.9%;
87.0%;
                       Last sequence update)
Last annotation update)
(EC 3.4.21.7).
                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAVY CHAIN A.
LIGHT CHAIN A.
KRINGLE 4.
KRINGLE 5.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 1;
Pred. No. 1.2e-10;
                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELAY SYSTEM
                                                                                                                                                       810 AA
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                                                                                                                                                                                                                                                                                                                                                                                      Indels
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-I- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEDLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLACENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES PIBRIN, FIBRONECTIN, THROMBOSPONDIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P., Byrne C.D., Fong K.J., Meer K., Patthy L.; "The recurring evolution of lipoprotein(a). Insights from cloning hedgehog apolipoprotein(a)."; J. Biol. Chem. 270:24004-24009(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erinaceus europaeus (Western European hedgehog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U33171; AAC48717.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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LAMININ AND VON WILLEBRAND FACTOR.
ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALDHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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IPR001254; Trypsin
0051; kringle; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001314; Chymotrypsin. IPR000001; Kringle. IPR003014; PAN.
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SMART; SM00130; KR; 5. SMART; SM00473; PAN_AP; 1. PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00018; KRINGLE. Pfam; PF00089; PF00024; trypsin; 1 PAN;

SMART; SM00473; PAN_AP; 1.
SMART; SM00020; TTYP_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1. Hydrolase; remodeling; Serine protease; Plasma; Glycoprotein; Fibrinolysis; 19 582 810 810 810 181 181 352 Blood coagulation; Kringle; Zymogen; PLASMINOGEN BY SIMILARITY.

Signal

DOMAIN DOMAIN DOMAIN CHAIN CHAIN DOMAIN 20 583 583 103 185 275 KRINGLE KRINGLE KRINGLE PLASMIN HEAVY CHAIN PLASMIN LIGHT CHAIN SERINE PROTEASE. (BY SIMILARITY).

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RESOLUTION AND ALL AND
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                                                                                                                                              Mikol V., Lograsso P.V., Boettcher B.R.;

*Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic acid: existence of novel and expected binding modes.*;

J. Mol. Biol. 256:751-761(1996).
MEDLINE=95002201; PubMed=7918682;
Scanu A.M., Pfaffinger D., Lee J.C., Hinman J.;
"A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37
associated with a lysine binding defect in Lp(a).";
                                                                                                                                                                                                                                                                                                                                                                                           Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet "Structural elucidation of the N- and O-glycans of human apolipoprotein(a): role of O-glycans in conferring protease
                                                                                                                                                                                                                                                                                MEDLINE=96217891; PubMed=8642595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salonen E.-M., Jauhiainen M., Zardi L., Vaheri A., Ehnholm C., "Lipoprotein(a) binds to fibronectin and has serine proteinase activity capable of cleaving it.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21303595; PubMed=11294842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The mysteries of lipoprotein(a).";
Science 246:904-910(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fless G.M., Scanu A.M., Lawn R.M.; "CDNA sequence of human apolipoprotein(a) is homologous to plasminoran ".
                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasminogen
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MCLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                  (-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
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PROSITE; PS50070; KRINGLE_2; 38
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
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SMART; SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              Kringle;
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HSSP; P00747; 1PMK.
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InterPro; IPR001254;
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-!- FUNCTION: Apo(a) is the main constit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteolytic fragmentation.
SIMILARITY: CONTAINS 38 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-Lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         naturally occuring proteolytic fragments is correlated with atherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structures present in either a mono- or disialylated state. 9
O-glycans are mostly (80%) represented by the monosialylated
type I structure, NeuNAcalpha2-3Galbeta1-3GalNAC, with smalle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LP(a)). It has serine proteinase activity and is able of autoproteolysis. Inhibits tissue-type plasminogen activator 1. LP(a) may be a ligand for megalin/Gp 330.
SUBUNIT: Disulfide-linked to apo-Bl00. Binds to fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Emburopean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: Elevated plasma concentrations of apo(a) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragments are competing with plasminogen for fibrin (ogen) binding.
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                                                                                                                                                                                                                                                                                                                                              Repeat;
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                                                                                                                                                                                                                                                                                                                                              Atherosclerosis;
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Polymorphism
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                   NA Schaller J., Straub C., Kaempfer U., Rickli E.E.;

(**Complete amino acid sequence of equine miniplasminogen.";

(**Complete amino acid sequence of equine miniplasminogen.

(**Complete amino acid sequence of equine miniplasminogen in South Dissource in Edward of the Fibria of Edward in South Internation in Arrivates the Urokaion,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse)
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    MISCELLANEOUS: PLASMIN IS INACTIVATED BY
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(Rel. 20, Last sequence update)
(Rel. 40, Last annotation update)
(EC 3.4.21.7) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Pred. No. 1.8e-08;
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W; 96921BE96A465C5F CRC64;
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PLMN_PIG
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Best Local S
Matches 18
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SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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                          SEQUENCE OF 1-560. Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E.; "Amino acid sequence of the heavy chain of porcine plasmin. Comp of the carbohydrate attachment sites with the human and bovine species."; Fibrinolysis 1:91-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLMN_PIG
P06867;
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
-!- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
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HSSP; P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, C
01-FEB-1991 (Rel. 17, I
16-OCT-2001 (Rel. 40, I
Plasminogen (EC 3.4.21.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.233;
                                                                                                                                                                                                                                NCBI_TaxID=9823;
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18; Conser
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nilarity 78.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                               06, Created)
17, Last sequence update)
40, Last annotation updat
.4.21.7).
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TRYPSIN_HIS; 1.
TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMIN LIGHT CHAIN B.

KRINGLE 5.

SERINE PROTEASE.

BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).
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Pred. No. 3.3e-09;
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8E9E56B5C5CDBE01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEAVY CHAIN A.
LIGHT CHAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         790 AA
                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 338;
                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNOWN AS
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SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
SMO0020; KRINGLE_1; 5.
PROSITE; PS00021; KRINGLE_2; 5.
PROSITE; PS50240; TRYPSIN_DOM; 1.
              CARBOHYD
                                                                                          DOMAIN
                                                                                                                       DOMAIN
                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE. SMART; SM00130; KR; 5.
                                                                          DOMAIN
                                                                                                                                                                                                 Tissue remodeling;
                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan.app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88185329; PubMed=3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85203907; PubMed=3846533;
Marti T., Schaller J., Rickli E.E.;
"Determination of the complete amino-acid sequence of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The N- and O-linked carbohydrate chains of human, bovine and plasminogen. Species specificity in relation to sialylation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlycoSuiteDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          miniplasminogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 450-790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fucosylation patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. BIOCHEM. 173:57-63(1988).

FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAPIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. SIMILARITY: CONTAINS 5 KRINGLE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAMININ AND VON WILLEBRAND FACTOR.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATORS BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, STALIC ACID IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARLDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICROHETEROGENEITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A25834; A25834.
S03733; S03733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem. 149:279-285(1985).
                                                                                                                                                                                                                                                                                                                                                                                        PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     PF00051; kringle; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00747;
                                                                                                                                                                                                                                  PS00135;
                                                                                                                                                                                                             Serine protease; Plasma; Glycoprotein; Fibrinolysis;
            561
561
84
166
256
256
358
358
461
461
602
740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P06867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5HPG.
                                                                                                                                                                                                                              TRYPSIN_SER;
                                                                                                                                                                                                                                             TRYPSIN_HIS; FALSE_NEG
                                                                                                                                                                                                 Blood
                                                                                                                                                                                                 coagulation;
         CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .
                                                                                     KRINGLE
KRINGLE
                                                                                                                                                  SERINE PROTEASE.
                                                                                                                                                                 PLASMIN HEAVY CHAIN A. PLASMIN LIGHT CHAIN B.
                                                                                                                                                                                                Kringle;
                                                                                                                                                                                                Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIALIC ACID AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           porcine
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RESULT 9
PLMN_BOVIN
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                           Trucosylation patterns.*;

(IL EUR. J. Biochem. 173:57-63 (1988).

(LL EUR. J. Biochem. 173:57-64 (1988).

(LL EUR. J. Biochem. 173:57-64 (1988).

(LL EUR. J. Biochem. 173:57-64 (1988).

(LA AUCTIONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,

(LA AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE

(LA AND INFLAMMATION; IN OVULATION OF THE UROKINASE-TYPE PLASMINOGEN

(LA ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH

AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,

(LAMININ AND VON WILLEBRAND FACTOR

(LAMININ AND VON WILLEBRAND FACTOR

(LAMININ AND VON WILLEBRAND FACTOR

(LAMININ AND TONESTED INTO PLASMIN BY PLASMINOGEN

ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO

(LETTING ACTIVATOR BE ACTIVATED WILL STREPTOKINASE.

(C. PIM: N-LINKED GLYCAN CONTAIN N-ACETYLLACTOSAMINE AND STALIC ACID

(C. PIM: N-LINKED GLYCAN CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS

MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEBOGENEITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P06868; Q28162;
01-JAN-1988 (ReJ
01-NOV-1997 (ReJ
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88185329; PubMed-3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
"The N- and O-linked carbohydrate chains of human, bovine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of a complementary human and bovine plasminogen."; Biochemistry 23:4243-4250(1984).
                                                                                                                                                                                                                                                                                                                                    plasminogen. Species specificity in relation to sialylation
                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85023311; PubMed=6148; Malinowski D.P., Sadler J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J., Kampfer U., Rickli E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berglund L., Andersen M.D., Petersen "Cloning and characterization of the Int. Dairy J. 5:593-603(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 706-812 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Co
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 149:267-278(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85203906; PubMed=3846532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 27-812,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLMN_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete amino acid sequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 RNPDGDDNGPWCYTTNPQKLFDY 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
IMMEDIATELY AFTER DISSOCIATION FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 06, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=6148961;
               PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.9%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113; DB 1;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-LINKED (GALNAC. . .).
/FTId=CAR_000020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davie E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F04EA06E74BCD58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.E.;
bovine plasminogen cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      812 AA
THE CLOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasminogen. Comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790;
                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                      porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  ΑS
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RESULT 10
PLMN_CANFA
ID PLMN C.
                                                     Qy
                                                                                                     멍
                                                                    Query Match
Best Local s
Matches 18
                                                                                                                                                                                                                                                                                                  Pfam; PF00051; kringle; 5.

Pfam; PF00024; PAN; 1.

Pfam; PF00089; Trypsin; 1.

Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

SMART; SM00130; KR; 5.

SMART; SM00473; PAN AP; 1.

SMART; SM00473; PAN AP; 1.

PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS500134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.
                                                                                                             CONFLICT
                                                                                                                           CONFLICT
                                                                                                                                          ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
PLMN_CANFA
                                                                                                     SEQUENCE
                                                                                                                                                                          CARBOHYL
                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GlycoSuiteDB; P06868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                      536
                                                     1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A25835; PLBO
                                      RNPDGDVNGPWCYTMNPRKPFDY 558
                                                                                                                                                                                                                                                                                                                                                                                                                                               P00747; 2P
S; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X79402; CAA55939.1; -. K02935; AAA30714.1; -.
                                                                     Similarity
18; Conser
                                                                                                                                                                                                                                                                              remodeling;
                                                                                                                                                                                                                                                                                              PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                        IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003014;
                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001314; Chymotrypsin.
                                                                                                     812
                                                                                                                                                                                                                                                                                      Serine
                                                                                                           624
667
762
335
516
744
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27
27
584
110
110
192
282
282
384
485
584
                                                                                                                                                                         365
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                                                                                                     Ā,
STANDARD;
                                                                                                                                                                                                                                                                                              TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                    protease;
                                                                                                                                                                                        26
812
583
812
188
269
269
359
461
564
812
                                                                                                                                                                                                                                                                              Blood
                                                                                                                    624
667
762
335
516
                                                                                                                                                                         365
                                                                                                    91216 MW;
                                                                            80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                 PAN.
                                                                                                                                                                                                                                                                              coagulation;
                                                                                                          SERINE PROTEASE.

N-LINKED (GLCNAC.
/FTId=CAR_000014.
O-LINKED (GALNAC.
/FTId=CAR_000015.
/FTId=CAR_X SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-> D (IN REF. 2).
O-> H (IN REF. 2).
P-> L (IN REF. 3).
                                                                                                                                                                                                                                                                            Plasma; Glycoprotein; Fibrinolysis; agulation; Kringle; Zymogen; Signal.
                                                                    1:
                                                                    Score 111; DB
Pred. No. 2.2e
1; Mismatches
                                                                                                                                                                                                       PLASMIN
PLASMIN
KRINGLE
KRINGLE
KRINGLE
KRINGLE
KRINGLE
PRT;
                                                                                                    38A6AA691E220946 CRC64;
                                                                                                          E RELAY SYSTEM.
E RELAY SYSTEM.
E RELAY SYSTEM.
D (IN REF. 2).
H (IN REF. 2).
L (IN REF. 3).
R (IN REF. 3).
                                                                                                                                                                                                                                             HEAVY CHAIN
333
                                                                            DB 1;
.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                   Length 812;
                                                                                                                                                                                                                                             ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
MBL outstation -
                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no
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      P80009;
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DISULFID
ACT_SITE
ACT_SITE
ACT_SITE
SITE
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DISULFID
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01-NOV-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_DM; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMININ AND VON WILLEBRAND FACTOR.

- LAMININ AND VON WILLEBRAND FACTOR.

- LAMININ BY PLASMINOGEN
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF STREPTOKINASE.

- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN. HSSP; P00747; 5HPG. MEROPS; S01.233; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90175323; PubMed=2626424;
Schaller J., Straub C., Kaempfer U., Rickli E.E.;
"Complete amino acid sequence of canine miniplasminogen.";
"Complete amino acid sequence of canine miniplasminogen.";
Protein Seq. Data Anal. 2:445-450(1989).

-i- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000001;
InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND INFLAMMATION; IN OVULLATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE URCKINASE-TYPE PLASMINGGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
                                                                                                                                                                                                                                                                                                                                                                                                                                           remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease; Plasma; Glycoprotein; Fibrinolysis;
  333
                                      104
25
54
90
100
130
222
222
279
145
2188
2183
2183
2183
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(Rel.
(Rel.
(EC 3.
AA;

    Created)
    Last sequence update)
    Last annotation update)
    Last annotation.

                                      Blood
36678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kringle.
Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                           coagulation; Kringle; Zymogen.
  ME
                            INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).

STREPTOKINASE-BINDING SITE (PROBABLE).
                                                                                                                                                                                                                                                                                  SERINE PROTEASE
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                              PLASMIN HEAVY CHAIN PLASMIN LIGHT CHAIN KRINGLE 5.
                  (BY SIMILARITY
  C8C0271B6C6AC8D4 CRC64;
                                                                                                                                                                                                                                                                                                                                            PROTEASE.
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RESULT TO SEE THE SEE 
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Best Local :
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                                                                                                                                                                                                                            EMBL; W74178; AAA50165.1; -.
EMBL; U37055; AAC50471.1; -.
EMBL; L11924; AAA59872.1; -.
PIR; A40331; A40331.
HSSP; P00747; 2PK4.
MEROPS; S01.975; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGFL HUMAN STANDARD; rm.,
P26927; Q1350; Q14870;
O1-AUG-1992 (Rel. 23, Created)
O1-AUG-1992 (Rel. 23, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSF) (Macrophage stimulating protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
"Cloning, sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3.";
J. Biol. Chem. 268:15461-15468(1993).
-I- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92002016; PubMed=1655021;
Han S., Stuart L.A., Friezner Degen S.J.;
"Characterization of the DNF1552 locus on human chromosome 3:
identification of a gene coding for four kringle domains with
homology to hepatocyte growth factor.";
Biochemistry 30:9768-9780(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                            InterPro;
                                                                                                  InterPro;
                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD I
HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEI
SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY. PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONSERVED.
                                                                                                                                                                                                              142408;
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                          PF00051;
PF00024;
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                                                                       ; IPR001314; Chymotry; IPR000001; Kringle.; IPR003014; PAN.; IPR003609; Pan_app.; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                          kringle; 4.
PAN; 1.
trypsin; 1.
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Primates;
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78.3%;
                                                                                                                                                                            Chymotrypsin.
                                                                                                  Pan_app.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
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RESULT 12
HGFL_MOUSE
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Best Local
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SMART; SM00473; PAN_AP; 1.

SMART; SM00020; TryP_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS502070; TRYPSIN_DOM: 1

Kringle; Glycoprotein; Serine pr
                                                                                  01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
16-OCT-2001 (Rel. 4
Hepatocyte growth f
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                                                                                                                              HGFL_MOUSE P26928;
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SEQUENCE
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CARBOHYD
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                               Eukaryota; Metazoa;
Mammalia; Eutheria;
            NCBI_TaxID=10090;
[1]
                                                   Mus musculus (Mouse)
                                                               MST1 OR HGFL.
                                                                        stimulatory protein)
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PR00018;
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                623
711
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                                                              .. 23, Created)
1. 23, Last sequence update)
1. 40, Last annotation update
th factor-like protein precur
tein) (MSP).
                                                                                                                                          STANDARD;
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80379 MW;
                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                   66.7%;
65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease
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SERIME PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                   /FTId=VAR_006631.
C -> F
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N-LINKED
Y -> C.
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KRINGLE
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                                                                                                                                                                                                                                                  Score 92; DB 1;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                  /FTId=VAR_006632.
L -> F (IN REF. 2).
596ED21F180290E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAP
                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRINGLE
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                                                                                                                                           716
                                                                                    update)
precursor
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                                                                                                                                                                                                                                                            Length 711;
                                                                                    (Macrophage
                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                          Indels
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THE PROPERTY OF THE PROPERTY O
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PRINTS; PRO0018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C; TISSUE-Liver:
MEDLINE-92007017; PubMed=1837957;
Friezner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
"Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor-like protein: expression during development.";
Biochemistry 30:9781-9791(1991).
-1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA CTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONSERVED.
TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUST BEFORE BIRTH THE LEVEL INCRESTABLE AFTERWARDS.
PTM: MAY BE CLEAVED AFTER AA 488,
HELD TOGETHER BY DISULFIDE BONDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M74181;
P00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00089
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                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003609; Pan_app
IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001314; Chymotrypsin. IPR000001; Kringle. IPR003014; PAN.
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AAA50167.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kringle; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hgf1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS 4 KRINGLE DOMAINS BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN_DOM;
        Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS EXPRESSED AT LOW LEVELS
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KRINGLE 4.

SERINE PROTEASE-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                               KRINGLE
KRINGLE
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KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO YIELD A TWO-CHAIN MOLECUL: OR CLEAVED INTO TWO SEPARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                homolog; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRAMATICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S1;
                                                                                                                                        SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLACENTA AND
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A Okajina A., Miyazawa K., Kitamura N.;
Primary structure of rat hepatocyte growth factor and induction of its mrNA during liver regeneration following hepatic injury.*;
Eur. J. Blochem. 193:375-381(1990).
C Eur. J. Blochem. 193:375-381(1990).
C IT HEPATOCYTE CELLS. SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
C IT HAS NO DETECTABLE PROTEASE ACTIVITY.
C IT HAS NO DETECTABLE PROTEASE ACTIVITY.
C IT SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A DISULFIDE BOND.
C IS SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
C ISSULLARITY: BELONGS TO PEPTIDASE FAMILY.
C TRYPSIN FAMILY. PLASMINOGEN SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel.
01-NOV-1990 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WISTAR; TISSUE-Liver; MEDLINE-90222197; PubMed=2139229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGF_RAT P17945;
                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of the mRNA in rat tissues.";
Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Deduced primary structure of rat hepatocyte growth factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toshiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatocyte growth (Hepatopoeitin A).
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D90102; BAA14133.1; X54400; CAA38266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Χ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l similarity
15; Conser
                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S., Nakamura T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
716 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hagiya M.,
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80588
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16, Last sequence update)
36, Last annotation update)
factor precursor (Scatter factor)
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INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

POTENTY

N-LINKED (GLCNAC. . .) (POTENTY

P -> Q (IN GENOMIC SEQUENCE).

MW; BBCE02EF85213ACC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimonishi M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
SIGNAL
                                                                                                                                 HGF_HUMAN STANDARD; PRT; 728 AA P14210; Q9UDU6; Q9BYL9; 01-JAN-1990 (Rel. 13, Created) 01-AUG-1991 (Rel. 19, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Hepatocyte growth factor precursor (Scatter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00021; KRINGLE_1; 4. PROSITE; PS50070; KRINGLE_2; 4. PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN
PRINTS; PR00018; KRINGLE.
                            SEQUENCE FROM N.A.
MEDLINE=91340155; PubMed=1831432;
MEDLINE=91340155; PubMed=1831432;
MEDLINE=91340155; PubMed=1831432;
MEDLINE=91340155; PubMed=1831432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00473; SMART; SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                 Seki T., Hagiya M., Shimoni "Organization of the human Gene 102:213-219(1991).
                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                  (Hepatopoeitin A).
HGF OR HPTA.
                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.978;
SEQUENCE FROM N.A
                                                                         NCBI_TaxID=9606;
                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                  442
                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                   1 RNPDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A35644; A35644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S13211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR001254;
PF00051; kringl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P14210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00024; PAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00130;
                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor; Kringle;
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003609;
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                                                                                                                                                                                                                                                                                                             AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KR; 4.
PAN_AP; 1.
                                                                                   ; Chordata;
; Primates;
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;le; 4.
                                                                                                                                                                                                                                                                                                             82905
                                                                                                                                                                                                                                                                              59.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Serine
                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                           hepatocyte
                                                                                                                                                                                                                                                                      Score 82; DB
Pred. No. 0.00
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         KRINGLE
KRINGLE
KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN HEPATOCYTE GROWTH FACTOR BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             3E0BF1F96ADCEDFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                   (Scatter factor) (SF)
                                     Nakamura T.,
                           growth
                                                                                                                                             update)
                                                                                                                                                                                                                                                                                         DB 1;
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                           T., Shimizu S.;
factor-encoding
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Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins Baker J.B., Godowski P.J.;

"Structure-function analysis of hepatocyte growth factor: identification of variants that lack mitogenic activity years affinity receptor binding.";

EMBO J. 11:2503-2510(1992).
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                                                                                                                                                                                                                                                                                           Yoshiyama Y., Arakakai N., Naka D., Takahashi K., Hirono S., Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T., Hishida T., Daikuhara Y.; "Identification of the N-terminal residue of the heavy chain native and recombinant human hepatocyte growth factor.";
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Arakaki N., Nakayama H., Hirono S.,
Gohda E., Daikuhara Y., Kitamura N.;
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                                                                                                                                                                                                                                                                               Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birchmeier W.; "Evidence for the identity of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Embryonic fibroblast;
MEDLINE-91334393; PubMed=1831266;
Meidner K.m., Arakaki N., Hartmann G.,
Rieder H., Fonatsch C., Tsubouchi H., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura T., Nishizawa T., Hagiya M.,
Sugimura A., Tashiro K., Shimizu S.;
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MEDLINE=91025062; PubMed=2145836;
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MEDLINE-93129192; PubMed=1482348;
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                                                                                                                                                                                                                                                                                                                                                                                                                 human hepatocyte growth factor gene.";
Biochemistry 30:9170-9176(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91369928; PubMed=1832556;
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                                                                                                                                                           189:1329-1335(1992)
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H., Ishii T.,
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MEDLINE=99936858; PubMed=9817840;
Ultsch M., Lokker N.A., Godowski P.J., de Vos A.
"Crystal structure of the NK1 fragment of human factor at 2.0-A resolution.";
Structure 6:1383-1393(1998).
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MEDLINE-98154323; PubMed-9493272;

Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,

Rubin J.S., Bottaro D.P., Byrd R.A.;

"The solution structure of the N-terminal domain of hepatocyte growth factor reveals a potential heparin-binding site.";
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SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A DISULFIDE BOND.
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M75975; AAG53460.1;
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AAA52648.1;
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PROSITE; PS00021; KRINGLE_1;
PROSITE; PS50070; KRINGLE_2;
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InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                         TISSUE=Mammary fibroblast;
MEDLINE=94183257; PubMed=8135822;
MEDLINE=94183257; PubMed=9418257; PubMed=
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MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.
"Structure, genetic mapping, and
factor gene.";
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InterPro; IPR000001; Kringle.
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Pan_app.
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                                                                                                                                                                                                                      Commun. 199:772-779(1994).
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KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
SERINE PROTEASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB Pred. No. 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                  expression of the mouse Hgf/scatter
                                                                                                                                                                                                                                                                                                                                                                                                       OF 496-504
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
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PROSITE; PS00701; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1
                                                                                                                                                                                                                                                                                               CHAIN
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                                                          CARBOHYD
                                                                         CARBOHYD
                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94060105; PubMed-8241272; Liu Y., Michalopoulos G.K., Zarnegar R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and characterization of cDNA encoding hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Adhes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restricted to the state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LONG FORM.
SIMILARITY: CONTAINS 4 KRINGLE DOMAINS
SIMILARITY: BELONGS TO PEPTIDASE FAMIL
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL IN IT HAS NO DETECTABLE PROTEASE ACTIVITY.

SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY DISULFIDE BOND.

ALTERNATIVE PRODUCTS: A SHORT FORM OF HGF IS PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:96079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE RNA SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S71816;
X72307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X72307; CAA51054.1; ALT_INIT.
P14210; 1BHT.
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                                                                                                                                                                                                                                                                                                                                                                      factor; Kringle;
                                                                                                                                                                                                                                                                                                                                                   Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001314; Chymotrypsin. IPR000001; Kringle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003609;
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AAB31855.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kringle; 4.
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BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
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 N-LINKED (
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KRINGLE
                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
HEPATOCYTE GROWTH FACTOR ALPHA CHAIN
                                                                                                          SERINE PROTEASE-LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                     INTERCHAIN (BY SIMILARITY)
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(GLCNAC. . .) (PO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as its content
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                  (POTENTIAL)
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RESULT 16
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21-JUL-1986
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE Magnusson S., Sottrup-Jensen L., Petersen T.E., Claeys H.; (In) Hemker H.C., Veltkamp J.J. (eds.); Boerhaave symposium on prothrombin and related coagulation fac pp.25-46, Leiden University Press, Leiden (1975).
                                                                                                        "The Ca2+ ion and membrane binding prothrombin fragment 1."; Biochemistry 31:2554-2566(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            "Three-dimensional structure of the prothrombin fragment 1."; Biochemistry 25:3977-3982(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MEDLINE=86296631; PubMed=3741841; Park C.H., Tulinsky A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-84203525; PubMed=6326805;
MCGillivray R.T.A., Davie E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
                          Martin P.D., Robertson W.,
                                          x-ray Crystallography (2.3 ANGSTROMS).
MEDLINE-92218459; Pubmed-1560020;
                                                                                                                                                                                           x-ray Crystallography (2.2 angstroms) MEDLINE=92190185; PubMed=1547238;
                                                                                                                                                                                                                                                                               Seshadri T.-P., Tulinsky A., Skra "Structure of bovine prothrombin resolution.";
                                                                                                                                                                                                                                                                                                                            MEDLINE=91311686; PubMed=1856869; Seshadri T.-P., Tulinsky A., Skrz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Mol. Biol.
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Mammalia; Eutheria;
                                                                                                                                                                           Soriano-Garcia M., Padmanabhan K.,
                                                                                                                                                                                                                                                             J. Mol.
                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 23:1626-1634(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of bovine prothrombin mRNA and product.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Irwin D.M., Robertson K.A., Macgillivray R.T.A.; "Structure and evolution of the bovine prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88245190; PubMed=3379642;
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in P.D., Robertson W., Turk D., Huber R., Bode W., Edward structure of residues 7-16 of the A alpha-chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNPDDDAHGPWCYTGNPLIPWDY 464
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RT "Characterization of the boulne prothrombin gene.";
RL BLOCHEMISTRY 24:6854-6861(1985).
RL BLOCHEMISTRY 24:6854-6861(1985).
CI FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CI FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS CONVERTS THE REMORE THE FORM THE FORM ACTIVATES FACTORS V, VII, VIII, XIII,
CI FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CI FIRST SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
CI FYM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CI FYM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CI FRESULT FROM THE CARBOXYGLUTAMYL RESIDUES BY A MICROSOMAL ENZYME, THE VITAMIN K-DEPENDENT CARBOXYGLES: THE MODIFIED RESIDUES
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
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CONTROL OF A CTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; V00135; CAA23451.1;
EMBL; J00041; AAA30781.1;
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"Refined 2.3 A X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors MAPAP, 4-TAPAP and MQPA. A starting point for improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of the thrombin complex with triabin, a lipocalin-like exosite-binding inhibitor derived from a triatomine bug."; proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
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SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                         European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.prozyme.com/technical/thrombindata.html"
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                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                      Bioinformatics Institute. The profit institutions as long
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Query Match
Best Local Similarity
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PROSITE; PS00011; GLU_CARBOXYLATION;
PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50040; TRYPSIN_DOM; 1.
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                                                                                                                                                                                                                                                                             PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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PRINTS; PR01505; PROTHROMBIN
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Pfam; PF00051; kringle; 2.
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S; PR00722; CHYMOTRYPSIN
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                                                                                                                                                                                                                                                     Serine
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                                                                                                                                                                                                                                                             Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-94
                                                                                                                   366
409
465
571
                                                                                                                                                                                                                                                                                                                                       GLA; 1
KR; 2.
                                                                                                                                                                                                                                                                                                                                                                        GLABLOOD.
                                                                                                                                                                                                                                                   protease; Kringle; Signal; 3D-structure.
                         58.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 VitK_dep_GLA
                                                                                                                                                                                                                                                                                                                                                                                                                         Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Prothrombin.
                              GAMMA-CARBOXYGLUTAMIC A
                                                                                                                CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                           ACTIVATION PEPTIDE (FRAGMENT ACTIVATION PEPTIDE (FRAGMENT THROMBIN LIGHT CHAIN (A)... THROMBIN HEAVY CHAIN (B).
                        N-LINKED
                                                                                                                                                                     SERINE PROTEASE
                                                                                                                                                                           KRINGLE
                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                            PROTHROMBIN
                        (GLCNAC.
        DB 1;
       Length 625
                                ACID.
                                                                                                                                                                                                                                                             Liver;
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No.

0.0005;

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RESULT 17
PLMN_RAT
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                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993
01-APR-1993
01-NOV-1995
Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLMN_RAT
Q01177;
                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DOMAIN
DISULFID
                              NON_TER
                                                PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.

PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.

PROSITE; PS00135; TRYPSIN_SER; PARTIAL.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
Tissue remodeling; Blood coagulation; Kringle.
                                                                                                                       Pfam; PF00051; kringle; 1. SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanalas J.J., Makker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                           InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                   PIR; A40522;
                                                                                                                                                                                           EMBL; M62832; AAA41884.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                     DOMAIN
                                                                                                                                                                MEROPS; SO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPDGSITGPWCYTTSP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNPDGDVGGPWAYTTNP 17
                                                                                                                                                                          P00747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 32, Last annotation update)
(EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                   A40522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
  10
112
>169
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
KRINGLE 3 (BY SIMILARITY).
KRINGLE 4 (BY SIMILARITY).
KRINGLE 5 (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169
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                                                                                                                                                                                                                                                                   gh a collaboration EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Best Local S
Matches 12
Query Match
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01-FEB-1994
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID NON_TER
                                                                                          NON CONS
NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00021; KRINGLE_1; 2
PROSITE: PS50070; KRINGLE_2; 2:
PROSITE: PS50240; TRYPSIN_DOM;
PROSITE: PS00134; TRYPSIN_HIS;
PROSITE: PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Plasminogen (EC 3.4.21.7) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00018; KRING
SMART; SM00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petromyzontiformes; Petromyzontidae; Petromyzon NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00051; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lamprey plasminogen.";
protein Seq. Data Anal. 5:207-211(1993).

-i- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUEMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00747; 1KRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation, characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Affolter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLMN_PETMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 RNPDNDQRGPWCFTTDPSVRWEY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNPDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY. $33879; $33879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND INFLAMMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
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                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRYPSIN_SER; PARTIAL.
protease; Plasma; Glycoprotein; Fibrinolysis;
Elood coagulation; Kringle; 2ymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28, Created)
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52.2%;
                                                                 35194 MW;
         52.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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PARTIAL.
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                                                                    1B5F0B539AC6ED3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
SIMILARITY
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            DВ
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banfield D.K., Macgillivray R.T.;

Banfield D.K., Macgillivray R.T.;

Partial characterization of vertebrate prothrombin cDNAs:

amplification and sequence analysis of the B chain of thrombin from

nine different species.";

1. PROCE. Matl. Acad. Sci. U.S.A. 89:2779-2783(1992).

1. FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

FIBRINGOEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,

AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

1. PRM: THE GAMMA-CARBOXYGLUTANYL RESIDUES, WHICH BIND CALCIUM IONS,

RESULT FROM THE CARBOXYGLUTANYL RESIDUES, WHICH BIND CALCIUM IONS,

RESULT FROM THE CARBOXYGLUTANYL RESIDUES BY A MICROSOMAL

ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES

ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION

OF THE CARBOXET OF THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
                  EMBL; X52835; CAA37017.1; -.
EMBL; M81397; AAA42240.1; -.
PIR; S10511; S10511
HSSP; P00734; 1UVS.
                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          This
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                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
MEROPS; S01.217; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92212913; PubMed=1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 383-617 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dihanich M., Monard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90332426; PubMed=2377469;
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                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                             OF PROTHROMBIN TO THROMBIN.

OF PROTHROMBIN TO THROMBIN.

MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITELLE HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of rat prothrombin."; ic Acids Res. 18:4251-4251(1990).
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                                                                                                                                                                       There are no restrictions ong as its content is in
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Best Local
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SMART; SM00130; KR; 2.

SMART; SM00130; Tryp_SPc; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50240; TRYPSIN_DOM; 1.
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PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Plasma, Calcium-binding; Glycoprotein; Repeat;
Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
Hydrolase; Serine protease; Kringle; Signal.
                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IPR001314; Chymotrypsin.; IPR002383; GLA_blood.; IPR002380; Kringle.; IPR003966; Prothrombin.; IPR001254; Trypsin.; IPR001254; VitK_dep_GLA.
                                  AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLABLOOD.
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                                590
70411
52.9%;
64.7%;
                                  MW;
                                         BY SIMILARITY.
Score 73; DB 1;
Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                           KRINGLE 1.
                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                           GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
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GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
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CLEAVAGE (BY FACTOR XA)
CLEAVAGE (BY FACTOR XA)
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                                                                                                                                                                                                                                                                                                                                                                                      CLEAVAGE
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                                                                                                                                                                                                 N-LINKED
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                                                                                                                                                                                                                                 GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE
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                                 AD27D1B71445DB1D CRC64;
                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
          Length 617;
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Matches

Similarity

Conservative

Mismatches

Indels

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RNPDGDVGGPWAYTTNP 17

159

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RESULT 20
THRB_MOUSE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nine different species.";

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

PROME OF THE PROME OF THE CLEAVES BONDS AFTER ARG & LYS, CONVERTS FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

PRIN: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESULT FROM THE CARBOX FROM THE CARBOXYLATION OF GLUTAMYL RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESULT FROM THE CARBOX FROM THE CARBOXYLATION OF GLUTAMYL RESULT FROM THE CARBOX FROM TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banfield D.K., Macgillivray R.T.; "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19221;
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Mammalia; Eutheria;
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                        PIR; A35827; A35827.
HSSP; P00734; 1B7X.
MEROPS; S01.217; -.
                                                                                                               EMBL; M81394; AAA40435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIV. BY FACTOR XA.

SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PHOSPHOLIPID MEMBRANE THAT INTOX THE FACTIONS; FACTOR XA REMOVES THE ACTIVATION PROTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR INTOXICE HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THROMBIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF PROTHROMBIN TO THROMBIN.
   MGI:88380;
                                                                                                                  X52308; CAA36548.1; -.
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A
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Last annotation
(EC 3.4.21.5).
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PROSTTE; PS00011; GLU_CARBOXYLATION;
PROSTTE; PS00021; KRINGLE_1; 2.

PROSTTE; PS50070; KRINGLE_2; 2.

PROSTTE; PS50240; TRYPSIN_DOM; 1.
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PRINTS; PR000722; CHYMOTRYPSIN
PRINTS; PR00001; GLABLOOD.
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SIGNAL
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PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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PF00051; kringle; 2.
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SM00130;
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p; IPR002383; GIA_blood.
p; IPR00001; Kringle.
p; IPR003966; Prothrombin.
p; IPR001254; Trypsin.
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Conservative
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KR; 2.
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CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC A
BY SIMILARITY.
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               Score 71; DB 1; Pred. No. 0.0099;
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N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...).
B89F719AAFD601E0 CRC64;
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                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=94350942; PubMed=8071320;
Rydel T.J., Yin M., Padmanabhan K.P., Bla
Correa P.E., Fenton J.W. II, Tulinsky A.;
"Crystallographic fermion of the property of the 
                                                                                                                                                                                                                                                                                                                                                      Rydel T.J.,
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Butkowski R.J., Elion J., Downing M.R.,
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J. Biol. Chem. 252:4942-4957(1977).
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MEDLINE=77193964; F
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"Nucleotide sequence of the gene
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                                                                                                                                                                                                                                  Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J., "The refined 1.9 A crystal structure of human alpha-thrombin: interaction with D-Phe-Pro-Arg chloromethylketone and significance
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"Crystallographic structure of human gamma-thrombin.";
J. Biol. Chem. 269:22000-22006(1994).
                                                                                                                                                                                                                                                                                               Roitsch C., Fenton J.W. II;
"The structure of a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO
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«-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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Hewett-Emmett D., Seegers W.H.;
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                                                                                               Blankenship D.T.,
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deoxyribonucleic acid and
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thrombin Quick II alters primary substrate Biochemistry 28:2078-2082(1989).
                       Miyata T.,
Iwanaga S.,
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Iwanaga S.;
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substitution of Glu-466 by Ala.";
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                                                                                                             "Prothrombin Salakta: substitution
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MEDLINE=99162521; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The thrombin E192Q-BPTI complex rearrangements: implications for
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Esmon C.T., Stubbs M.T.;
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MEDLINE=97357286; PubMed=9214615;
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                                                                                     the fibrinogen clotting istry 31:7457-7462(1992)
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                                      Morita
             Tokushima, a replacement of arginine-418
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                                   PubMed=3567158; T., Inomoto T.,
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O M., Kumabashiri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Detection of a single base substitution of the gene for prothrombin Tokushima. The application of PCR-SSCP for the genetic and molecular analysis of dysprothrombinemia.";
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Transfer for the content of th
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MEDLINE=92256895; PubMed=1349838;
                                                                                                                                                                                                                                                                                                            between
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PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,

RESULT FROM THE CARBOXYGLUTAMYL RESIDUES BY A MICROSOMAL

ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES

ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Haematol. 54:245-254(1983).
FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C. SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                            NOT OCCUR IN PLASMA.
SIMILARITY: CONTAINS 2 KRINGLE DO
SIMILARITY: BELONGS TO PEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PRETIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                    TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO BY FACTOR XA.
MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVAL PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEAS NATURAL BLOOD CLOTTING.
MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF PROTHROMBIN TO THROMBIN.
DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS
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  InterPro; IPRO00001; Kringle.
InterPro; IPRO01254; Trypsin.
Pfam; PF00051; kringle; 10.
Pfam; PF00089; trypsin; 1.
SMART; SM00130; KR; 10.
SMART; SM00120; Tryp.SPc; 1.
SMART; SM00020; Tryp.SPc; 1.
PROSITE; PS00021; KRINGLE_1; 9.
PROSITE; PS00021; KRINGLE_2; 10.
PROSITE; PS50070; KRINGLE_2; 10.
PROSITE; PS500134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FAL
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J. Biol. Che
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01-MAR-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein(a) (EC
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                                                                                                                             DOMAIN
                                                                                                                                                        NON_TER
                                                                                                                                                                                                                              PROSITE; PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Rhesus monkey apolipoprotein(a). Sequence, evolution,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naturally occurring proteolytic fragments is correlated with atherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding. MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-L(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation (By similarity). SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRANSLEY TO THE TRANSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     decorin (By similarity).
PTM: N- and O-glycosylated (By similarity).
DISEASE: Elevated plasma concentrations of apo(a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoproteolysis. Inhibits tissue-type plasminogen activator Lp(a) may be a ligand for megalin/Gp 330. SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A30848; A30848.
A32869; A32869.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J04635;
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13, Last sequence update)
41, Last annotation update)
(EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).
                                                                                                                                                                                                      protease; Lipid transport;
                                                                                                                                                                                                                              TRYPSIN_DOM; 1.
TRYPSIN_HIS; FALSE_NEG.
TRYPSIN_SER; FALSE_NEG.
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Plasma; Glycoprotein;

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                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Batter R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 48.2 kDa protein Rv1490.
RV1490 OR MT1536 OR MTCY277.12.
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                                                                                    Hypothetical
                                                                                                                                      TIGR; MT1536;
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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P71771;
                                                             RANSMEM
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                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                      Z79701; CAB02040.1;
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van Bokhoven H., Celli J., Kayserili H., van Beusekom E. Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., "Mutation of the gene encoding the ROR2 tyrosine kinase autosomal recessive Robinow syndrome."; Nat. Genet. 25:423-426(2000).
                                                                                                                                                                                                                                        wilkie A.O.M., Jeffery S.;
"Recessive Robinow syndrome, allelic
is caused by mutation of ROR2.";
                                                                                                                                 MEDLINE-20392395; PubMed=10932187;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=20392394; PubMed=10932186; Afzal A.R., Rajab A., Fenske C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       brachydactyly type B.";
Am. J. Hum. Genet. 67:822-831(2000).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tyrosine-protein kinase transmembrane receptor RoR2 precursor
(EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).
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                                                                                                                                                                                                                                                                                                                           Ternes-Pereira E.,
                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS RRS C-184; W-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause brachvdactvly type B.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oldridge M., Fortuna A.M., Maringa M., Propping P., Mans Pollitt C., DeChiara T.M., Kimble R.B., Valenzuela D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mundlos S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Dominant mutations in ROR2, encoding an orphan receptor tyrosine kinase, cause brachydactyly type B.";
Nat. Genet. 24:275-278(2000).
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Mammalia; Eutheria; Primates; Catarrhini;
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16-OCT-2001 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel family of cell surface receptors with tyrosine kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROR2 OR NTRKR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 PHGMVENPWAVATTPQRVLDY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PDGDVGGPWAYTTNPRKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                    25:419-422(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09нв61;
                                                                                                                                                                                                                                                                                                                        Tueysuez B., Murday V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.5%;
47.6%;
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                                                                                                                                                                                                                                                                                                                  Fenske C.D., Oldridge M., Elanko N., evsuez B., Murday V.A., Patton M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.
                                                                                                                                                                                                                                                                                                                                                                                                     W-366 AND K-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144B549CD418F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                 to dominant brachydactyly type B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mansour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolff G.,
                                                                                                      .
H
                                                       Brunner
causes
                                                                                                           Balci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pfam; PF01392; Fz; 1.
Pfam; PF00041; ig; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [6]
ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPOSINE Phosphate.

1. SUBCELLULAR LOCATION: Type I membrane protein.

2. DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.

2. IDISEASE: DEFECTS IN ROR2 ARE A CAUSE OF BRACHYDACTYLY TYPE B REPAIR OF THE AN AUTOSOMAL DOMINANT SKELEFAL DISORDER OF BRACHYDACTER AND NAILS. IN BDB IS AN AUTOSOMAL DOMINANT SKELEFAL DISORDER AND NAILS. IN BDB THE MIDDLE PHALANGES ARE SHORT BUT IN ADDITION THE TERMINAL PHALANGES ARE RUDIMENTARY OR ABSENT. BOTH FINGERS AND TOES ARE PHALANGES ARE RUDIMENTARY OR ABSENT. BOTH FINGERS AND TOES ARE AFFECTED. THE THUMBS AND BIG TOES ARE USUALLY DEFORMED.

2. DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF RECESSIVE ROBINOW SYNDROME AFFECTED BY SKELETAL DYSPLASIA WITH GENERALIZED LIMB BONE SHORTENING, SEGMENTAL DEFECTS OF THE SPINE, BRACHYDACTYLY AND A DYSMORPHIC FACIAL APPEARANCE.

2. SIMILARITY: CONTAINS 1 FRIZILED (FZ) DOMAIN.

3. SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

3. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.

4. BEYONGS TO THE ROPE SIRPANHIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S., Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.; Nat. Genet. 26:383-383(2000).

1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAY BE INVOLVED IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS TO BE
                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                         InterPro;
                                                                                                                                                         InterPro;
                                                                                                                                                                          InterPro;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                        InterPro;
                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN. BELONGS TO THE ROR SUBFAMILY.
                                                                                                                                                                                                                        268310;
                                                                                                                                                                                                                                                                                                                                  AF279756;
AF279757;
AF279758;
                                                                                                                                                                                                                                         113000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF254749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M97639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF254748;
             SM00408;
SM00130;
                                                                                                                                                                       IPR000719;
IPR000024;
IPR003006;
                                                                                                                          IPR001245;
                                                                                                                                          IPR000001;
                                                                                                                                                         IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA60276
                                                                                                                                                                                                                                                                     1KRN.
                                                                                                                                                                                                                                                                                                                                                                AAG33132.1;
AAG33132.1;
AAG33132.1;
                                                                                                                                                                                                                                                                                                                                                                                                              AAG01184.2;
AAG01184.2;
AAG01184.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG01184.2;
AAG01184.2;
AAG01184.2;
AAG01184.2;
AAG01184.2;
           IGC2; 1.
KR; 1.
                                                                                                                                                                                                                                                                                                                                  AAG33132.1;
AAG33132.1;
 TyrKc; 1.
                                                                                                                                         Ig_MHC.
Ig_c2.
Kringle.
                                                                                                                          Tyr_pkinase
                                                                                                                                                                                         Euk_pkinase.
Fz_domain.
                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
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JOINED.
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RESULT 25
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                               Query Match
Best Local
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17yrosine-protein kinase transmembrane receptor ROR2 precursor (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related Creaters)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Tyrosine-protein kinase; ATP-binding; Receptor; Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Developmental protein; Polymorphism;
                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         Q9Z138;
                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                 NCBI_TaxID=10090;
                                                                                                                                  ROR2_MOUSE
SEQUENCE FROM N.A
                                                                 mROR2).
                                                                                                                                                                                 366 RNPGGQMEGPWCFTQN 381
                                                                                                                                                                                                    1 RNPDGDVGGPWAYTTN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation.
                                                                                                                                                                                                                       Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50038; FZ; 1.
PS00021; KRINGLE_1; FALSE_NEG
PS50070; KRINGLE_2; 1.
PS00107; PROTEIN_KINASE_ATP;
PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                             943 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                169
316
473
753
784
859
479
507
615
646
83
                                                                                                                                                                                                                                                                                                 620
                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                              182
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               245
                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                             104726
                                                                                                                                                                                                                                42.8%;
                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
C-> Y (IN RRS).
                                                                                                                                                                                                                                                                                 R -> W (IN RRS).

/FTId=VAR_010770.

N -> K (IN RRS).

/FTId=VAR_010771.

V -> I.
                                                                                                                                                                                                                                                                                                                                              R -> C (IN RRS).
/FTId=VAR_010768.
R -> W (IN RRS).
/FTId=VAR_010769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FALSE_NEG
                                                                                                                                                                                                                                Score 59; DB 1; Length 943; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-) (BY SIMILARITY). BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
TYROSINE-PROTEIN KINASE TRANSMEMBRANE
RECEPTOR ROR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       A ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                             /FTId=VAR_010913.
; DBAC1E4622B5ECA0 CRC64;
                                                                                                                                                                                                                                                                                                                            /FTId=VAR_010912.
                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_010911.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FALSE_NEG
                                                                                                                                     944 AA
                                                                             receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                          0;
                               Mus
                                                                              ی
                                                                                                                                                                                                                          Gaps
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0,

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SMART; SM00408; IGC2; 1.

SMART; SM00130; KR; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS50038; FZ; 1.

PROSITE; PS50021; KRINGLE_1; FALSE_NEG.

PROSITE; PS50070; KRINGLE_2; 1.

PROSITE; PS50070; KRINGLE_2; 1.

PROSITE; PS500107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J. Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.; "Spatio-temporally regulated expression of receptor tyrosine kinases, mRorl, mRor2, during mouse development: implications in development and function of the nervous system.";
DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00018; KRINGLE. PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Ror2, encoding a receptor-like tyrosine kinase, is required for cartilage and growth plate development.";
Nat. Genet. 24:271-274(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99248426; PubMed=10231392; Oishi I., Takeuchi S., Hashimoto R
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB010384; BAA75481.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
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                                                                                                    DOMAIN
                                                                                                                                                                    Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20164325; PubMed=10700181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Ror2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valenzuela D.M., Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro;
                                                                                                                                                           mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                             1; PF01392; Fz; 1.
n; PF00047; ig; 1.
n; PF00051; kringle; 1.
n; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAIN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEM REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1347521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cells 4:41-56(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003598; Ig_c2.
IPR000001; Kringle.
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000024; Fz_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
34
404
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76
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316
473
753
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                                                                                                                                                            domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ror2
403
424
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303
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782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euk_pkinase.
                                                                                                                                                           Developmental
SER/THR-RICH
                                                                       CYTOPLASMIC (POTENTIAL)
             PROTEIN KINASE
                              KRINGLE
                                                                                                  EXTRACELLULAR
                                                                                                                              TYROSINE-PROTEIN KINASE TRANSMEMBRANE
                                                                                                                  RECEPTOR ROR2
                                                         IG-LIKE C2-TYPE
                                                                                                                                               POTENTIAL
                                                                                                                                                           protein.
                                                                                                  (POTENTIAL)
                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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01-JUL-1989
                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and partitions as long as its content modified and this statement is not removed. Usage by and partitions as light as a light statement is not removed.
                                                                                                                                                          -!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
-!- PTM: THE SINCLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue-type plasminogen activator precursor (t-PA) (t-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator mRNA and its expression during F9 teratocarcinoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickles R.J., Darrow A.L., Strickland S.;
"Molecular cloning of complementary DNA to mouse tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88087303; PubMed=2826484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                  BIOL Chem. 263:1563-1569(1988).
FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN.
TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
CATALYTIC ACTIVITY: Specific cleavage of Arg-I-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTN
                                                                                                                                                                                                                                                                                                                                     plasminogen to form plasmin. SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                    TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                          BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 11, Created)
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56.2%;
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Pred. No. 0.83;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                           CAN BE FURTHER
                                                                                                                   a collaboration
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or send an email to license@isb-sib.ch).

EMBL; J03520; AAA40470.1;

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There are no restrictions ong as its content is in

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Matches 12
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SMART; SM00058; FN1; 1.

SMART; SM00058; KR; 2.

SMART; SM00100; Tryp_Spc; 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS0123; FIBRONECTIN 1; 1.

PROSITE; PS00021; KRINGLE 1; 2.

PROSITE; PS00020; KRINGLE 2; 2.

PROSITE; PS00014; TRYPSIN_DM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00722; ČHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM000181; EGF; 1.
SMART; SM00058; FN1; 1.
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen
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266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n; PF00008; EGF; 1.
n; PF00039; fn1; 1.
n; PF00051; kringle; 2.
n; PF00089; trypsin; 1.
RNPDGD-ARPWCHVMKDRKLTWEY
                          RNPDGDVGGPWAYTTNPRKL-YDY 23
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S01.232;
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IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97610; Plat.
IPR001314; Chymotrypsin.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000083;
                                                                                                              activation; Hydrolase; Serin
ngle; EGF-like domain; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309
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308
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Trypsin.
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                                                                   40.6%;
                                                                                                               W.
                                                                                                        CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY 
                                                     Score 56; DB Pred. No. 1.3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE.
KRINGLE 1.
KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                KRINGLE 2.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE
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                                                                    DB 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMINOGEN
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PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease;
                                                                                1;
                                                                                Length 559;
                                                                                                                           .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATOR.
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EMBL; EMBL; EMBL; EMBL;

AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1; AAA42261.1;

EMBL; EMBL;

AAA42261. AAA42261.

AAA42261.1; AAA42261.1;

EMBL;

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TPA_RESULTY
TPA_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOND.

BOND.

SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.

PTM. THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHE PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.

MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN, BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 2 KRINGLE DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990).

-I- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN. TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

-I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-I- SUBBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequen
16-OCT-2001 (Rel. 40, Last annota
Tissue-type plasminogen activator
(t-PA) (t-plasminogen activator).
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                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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"The
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DNA 7:671-677(1988).
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MEDLINE=89170114; PubMed-3148445;
NY T. Leonardsson G., Hsueh A.J.
"Cloning and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116
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AAA42261.
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20, Last sequence up
40, Last annotation
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a cDNA for rat tissue-type
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BOND IN PLASMINOGEN. BY
IT PLAYS AN IMPORTANT
IN CELL MIGRATION AND
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SMART; SM00130; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS001022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS0123; FIBRONECTIN_1; 1.

PROSITE; PS0123; KRINGLE_1; 2.

PROSITE; PS00013; KRINGLE_2; 2.

PROSITE; PS50040; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_TSR; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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PRINTS; PR00018; KRINGLE.
SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
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PIR; A35029; A35029.
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                                                                                                   Local
                     1 RNPDGDVGGPWAYTTNPRKL-YDY 23
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IPR000001;
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559 AA;
                                                                             Conservative
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fibronectin_type_1.
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CHARGE RELAY SYSTEM.
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                                                                                             Score 56; DB Pred. No. 1.3;
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                                                                     Mismatches
                                                                                                                        DB 1;
                                                                        7;
                                                                                                                      Length 559;
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RESULT 29
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PHLN_BURPS
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Best Local S
Matches 12
                                                                                                                    TPA_HUMAN STANDARD; PRT; 562 AA. P00750; Q15103; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Tissue-type plasminogen activator precursor (EC 3.4.21.68) (t.PA) (t.PA) (t.PA) (t.PA) (t.PA) (t.PA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF107252; AAF17299.1; -. Hydrolase; Signal. Signal 19 PO
                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of a nonhemolytic phospholipase C from Burkholderia pseudomallei.";
J. Clin. Microbiol. 37:3742-3745(1999).
-!- FUNCTION: HYDROLYZES PHOSPHATIDYLSERINE AS WELL AS
TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
             SEQUENCE FROM N.A
                                             NCBI_TaxID=9606;
                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Non-hemolytic phospholipase C precursor (EC 3.1.4.3) (PLC-N)
(Phosphatidylcholine cholinephosphohydrolase) (Phosphatidylcholine-
hydrolyzing phospholipase C) (PC-PLC).
                                                                                                                                                                                                                                                                                                           548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99454884; PubMed=10523590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria, Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burkholderia pseudomallei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHLN_BURPS
                                                                                                                                                                                                                                                                                                                                      7 VGGPWAYTTNPRK-----LYD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diacylglycerol + choline phosphate.
SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                      l Similarity
12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                      700
.; 77190 MW;
                                                           Primates; Catarrhini; Hominidae;
                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                    38.0%;
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5; D
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NON-HEMOLYTIC PHOSPHOLIPASE C. 5EDAE6FCD0FB129B CRC64;
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Harris T.J., Polickaert G., Rombauts W., Billiau A.,
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Ny T., Elgh F., Lund B.;
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                            TISSUE=Melanoma;
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               MEDLINE=85000468; PubMed=6433976;
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plasminogen activator
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REFERENCE PROPERTY OF THE PROP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91244765; PubMed-1645336; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., B Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., B "Disulfide pairing of the recombinant kringle-2 domain plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991).
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MEDLINE=91159408; PubMed=1900431;
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"Tissue plasminogen activator has an O-linked fucose attached
threonine-61 in the epidermal growth factor domain.";
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MEDLINE=90192129; PubMed=2107528;
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"Carbohydrate structure of recombinant human uterine tissue
plasminogen activator expressed in mouse epithelial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The 2.3 A crystal structure of the catalytic domain two-chain human tissue-type plasminogen activator."; J. Mol. Biol. 258:117-135(1996).
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Biochemistry
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                                                                                                                                                                  STRUCTURE BY NMR OF KRINGLE
                                                                                                                                                                                                                     "crystal structure of the kringle 2 domain activator at 2.4-A resolution."; Blochemistry 31:270-279(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
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                                                                               IH NMR structural characterization of a recombinant kringle
                         human tissue-type plasminogen activator."; nemistry 28:9350-9360(1989).
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                                                                                                   99; PubMed=2558718;
Kelley R.F., Llinas M.;
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melanoma cell plasminogen
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RESULT 30
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ID Y4HQ_R
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DE Hypoth
GN Y4HQ.
OS Rhizob
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01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 21.7 kDa protein Y4HQ.
                                                                                                                                                       Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium.
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-i- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN.
TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
     Rochepeau P.,
                                               "Molecular basis of symbiosis Nature 387:394-401(1997).
                                                                                            Freiberg C.A., Fellay R.,
                                                                                                             MEDLINE=97305956; PubMed=9163424;
                                                                                                                            SEQUENCE FROM N.A.
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                  SEQUENCE OF 1-52 FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Downing A.K., Driscoll P.C., Harvey T.S., Dudgeon T.J., Smith B.O., Baron M., Campbell I.D.;
"Solution structure of the fibrin binding finger domain of tissue-type plasminogen activator determined by 1H nuclear magnetic
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"Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
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MEDLINE=92292163; PubMed=1602484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91200042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RNPDGDVGGPWAYTTNPRKL-YDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasminogen to form plasmin. SUBUNIT: BINDS TO FIBRIN WITH HIGH AFFINITY. THIS INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
CATALYTIC ACTIVITY: Specific cleavage of Arg-)-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                   RNPDGD-AKPWCHVLKNRRLTWEY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. 225:821-833(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Fellay R.,
                                                                                                                                                                                                                          (strain NGR234).
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197:155-165(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7582899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=1901789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%;
Broughton W.J.;
                                                                                            Bairoch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52;
                                                               between
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                      194
                                                            Rhizobium and legumes.";
                                                                                         Broughton W.J., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                Hydrolase;
SIGNAL
                                          Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                            modified and this statement is not removed. Usage by are entities required a licens.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                             Ono M., Swanson J.J., Field L.M., Devonshire A.L., Siegfried B.D.;
"Amplification and methylation of an esterase gene associated with
insecticide-resistance in greenbugs, Schizaphis graminum.";
Insect Biochem, Mol. Biol. 29:1065-1073(1999).

-i- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.

-i- CATALUTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHGA
                                                                                                          EMBL; Y17580; CAA76792.1; -
                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                         InterPro; IPR002018; Carboxylesterase_B
                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THIS ESTERASE CONFERS OF INSECTICIDE RESISTANCE.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 22-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=13262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; 
Aphidiformes; Aphidoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizaphis graminum (Aphid).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20078165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Esterase SG1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X74068; CAA52198.1; ALT_INIT. EMBL; AE000077; AAB92455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO A.RHIZOGENES PLASMID PRIA4B ORE-3 IN VIRA REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            981429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-DEC-1998
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                                                                                                                                                                                                                                                                                                                     carboxylic anion.
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                           Serine esterase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
es; Aphidoidea; Aphididae; Aphidini; Schizaphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
1 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10612041;
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72.7%;
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Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647B7161AF1513E3 CRC64;
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                                                           PARTIAL
                            Signal
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RESULT 32
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    THE TETRET TETRET OF A DESCRIPTION OF A 
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Best Local
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p35501;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
01-OCT-1994 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID CARBOHYD CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
01-OCT-1994 (Rel. 30, Last annotation update)
Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).
Myzus persicae (Peach-potato aphid).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYZPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance in the peach-potato aphid, Myzus Biochem. J. 294:569-574(1993).
-i- FUNCTION: OVERPRODUCTION OF NONSPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyn
Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus
                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; x74554; CAA52648.1; PIR; S36786; S36786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93384534; PubMed=8373371; Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.; "Cloning and analysis of the esterase genes conferring ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 24-63 STRAIN-R3 / ISOLATE 794J;
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                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                               PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1
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InterPro; IPR000379; Est_lip_thioest_actsite
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                           CARBOHYD
                                              CARBOHYD
                                                                     CARBOHYD
                                                                                            CARBOHYD
                                                                                                                DISULFID
                                                                                                                                     DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.

CATALTYTC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDIAGGYEYTYSGRKIYSF 50
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                                                                                                                                                                                                                                                                                             PS00941;
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                                                                                                                                                                                                                                                                                                                                      COesterase;
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                                                                                                                                                                                                                                                                                             CARBOXYLESTERASE_B_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.1%;
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N-LINKED (GLCNAC. . . .

A -> T (IN REF. 1; AF

R -> N (IN REF. 1; AF
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                                                                                                                                                                                                                                                                      Glycoprotein;
ESTERASE E4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                               FALSE_NEG.
                                                                                                                                                                                                                                                                        Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sternorrhyncha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA SEQUENCE).
AA SEQUENCE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ьy
                                                                       (POTENTIAL).
                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Sulzer).";
                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alcohol +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYZPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and analysis of the esterase genes resistance in the peach-potato aphid, Myzus Biochem. J. 294:569-574(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CT-1994 (Rel. 30, Last annotation update)
Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).
                                                                                                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
-i- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 = an alcohol + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93384534; PubMed=8373371;
                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ISOLATE 800F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myzus persicae (Peach-potato aphid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTF_MYZPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=13164;
                                                                                       CARBOHYD
                                                                                                   CARBOHYD
                                                                                                               CARBOHYD
                                                                                                                                                                                                                              PROSITE; PS00122; PROSITE; PS00941;
                                                                                                                                                                                                                                                                                               HSSP; P21836; 1MAA.
                                                                                                                                                                                                                                                                                                                    EMBL; X74555; CAA52649.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                    ACT_SITE
                                                                                                                                                               ACT_SITE
                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                        Pfam; PF00135; COesterase;
                                                                                                                                                                                                                                                                     InterPro; IPR000379; Est_lip_thioest_actsite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GEIAGGFEYTYNGRKIYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carboxylic anion
                                                                                                                                                                                                                                                                                                         S36787; S36787.
                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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8; Conserv
Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 AA;
                                                                                                                                                                                                                                                                                IPR002018; Carboxylesterase_B
                                                                                                                                                                                                                   Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                  564 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                     esterase;
                                                                                                                                                                                                                                CARBOXYLESTERASE_B_2; FALSE_NEG
                                                                                                                                                                                                                                              CARBOXYLESTERASE_B_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND SEQUENCE OF 24-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61348 MW;
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42.1%;
                                                  62757 MW;
            42.1%;
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Pred. No. 6.
                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                       ESTERASE FE4.
BY SIMILARITY
BY SIMILARITY
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BY SIMILARITY
BY SIMILARITY
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N-LINKED
N-LINKED
N-LINKED
             Pred. No.
                         Score 51;
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                                                    128CC0EC3F2D9F1A CRC64;
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LINKED (GLCNAC. .
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6.8;
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              9
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persicae (
                                                                                                                                                                                                                                                                                                                                                                          Usage by and for commercial
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                            Length 564;
                                                                                                                .) (POTENTIAL).
  Indels
                                                                            ) (POTENTIAL)
) (POTENTIAL)
) (POTENTIAL)
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Matches

Conservative

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Mismatches

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RESULT 34
TPA_BOVIN
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Pfam: PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; tryps1;; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SM0018; EGF; 1.
SMART; SM00086; FN1; 1.
                                                                                                                                      InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q28198;
                                                                                                                                                                                                                                      EMBL; X85800;
HSSP; P00750;
                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tissue-type plasminogen activator precursor (EC
                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (t-PA) (t-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.

PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OF FACTOR XA.

MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.

CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.

SIMILARITY: CONTAINS 1 EFF-LIKE DOMAIN.

SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN TO PLASMIN BY HUDROLIZING A SINCLE ARG-VAL BOND IN PLASMINOGEN. BY CONTROLLING PLASMIN-MEDIATED PROTECLYSIS, IT PLAYS AN INFORTANT ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND MANY OTHER PHYSIOPATHOLOGICAL EVENTS.

CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen to form plasmin.
SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tPA."
                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dairy J. 5:605-617(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIAGGFEYTYNGRKIYSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                        S01.232;
                                                                                                                               IPR000001; kringle.
IPR001254; Trypsin.
IPR000083; fibronectin_type_1.
                                                                                                                                                                                     IPR000561; EGF-like
                                                                                                                                                                                                  IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                      CAA59795.1; -.
                                                                                                                                                                                                                                        1RTF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora;
                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
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Best Local
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PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01253; FIBRONECTIN_1;

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 2.

PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Chiroptera; Microchiroptera;
                                                                   Desmodus rotundus (Vampire bat).
Desmodus rotundus (Vampire bat).
Permora: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Desmodus in the lateral control of the lateral c
                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Salivary plasminogen activator gamma precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID DISULFID
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ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                              gamma)
                                                                                                                                                                                                                         URTG_DESRO P49150;
                                 NCBI_TaxID=9430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00130; KR;
SMART; SM00020; Tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasma; Kringle; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen
                                                                                                                                                                                                                                                                                                                                    272 RNPDGD-AQPWCHVWKDRQLTWEY 294
                                                                                                                                                                                                                                                                                                                                                                        1 RNPDGDVGGPWAYTTNPRKL-YDY 23
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70
87
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111
                                                   Desmodus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487
63701
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45.8%;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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BY SIMILARITY.

BY SIMILARITY.

TISSUE-TYPE PLASMINOGEN I
TISSUE-TYPE PLASMINOGEN I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-I. EGF-LIKE.
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                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·LINKED (GLCNAC. . .) (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
2EB6BEB4E32276C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease;
                                                                                                                                                                                                                                       394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 566;
                                                                                                                                          (EC 3.4.21.68) (DSPA
                                                                 Phyllostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATOR
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MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W.,
Kraetzschmar J., Haendler B., Langer G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vampire bat): unique fibrin specificity.";
ann. N.Y. Acad. Sci. 667:395-403(1992).
-i- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE
EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kraetzschmar J., Haendler B., Langer G.,
Alagon A., Donner P., Schleuning W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Salivary
                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                   SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE: PS50070; KRINGLE_2; 1.
PROSITE: PS50240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M63990; AAA31595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Plasminogen activators from the saliva of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donner P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alagon A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92039036;
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00051; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000001; Kringle.
InterPro; IPR001254; Trypsin.
                                DISULFID
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                                                                                                                                                     ACT_SITE
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                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                               Kringle;
                                                                                                                                                                                                                                                             Plasminogen activation;
                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin;
                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced throu-
ween the Swiss Institute of Bioinformatics and the
European Bioinformatics Institute. There are no re-
by non-profit institutions as long as its conten-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Specific cleavage plasminogen to form plasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P98119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                S01.
                                                                                                                                                                                                                                                                       PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                              Signal; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001314; Chymotrypsin.
                   142
1189
238
345
66
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131
174
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308
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       44105
                                                                                                                                                                                                                                                            Hydrolase; Serine protease; Glycoprotein;
        ₹
CHARGE RELAY SYSTEM (BY SI)
BY SIMILARITY.
                                                                                                                                                                                                                                                family.
                                                                                                                                                                                                            KRINGLE
                                                                                                                                                                                                                       SALIVARY PLASMINOGEN ACTIVATOR GAMMA
                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It is produced through a collaboration
                                                                                                                                                                                               PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bringmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rotundus (common
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/ SIMILARITY)
/ SIMILARITY)
                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               commercial
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Query Match

36.6%;

Score 50.5;

DВ

Length 394;

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RESULT 36
FA12_HUMAN
AT THE REPORT OF THE THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cool D.E., Edgell C.-J.S., Louie (
McGillivray R.T.A.)
"Characteriant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cool D.E., McGillivray R.T.A.;
Characterization of the human blood coagulation factor XII gene.
"Characterization and analysis of the 5'-flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00748; P78339;
21-JUL-1986 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88007593; PubMed=2888762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction of the primary structure
structure of beta-factor XIIa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 14-615 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tripodi M., Citarella F., Guida Cortese R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 4-615 FROM N.A. MEDLINE=86176794; PubMed=3754331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of human blood coagulation prediction of the primary structure of factor
                    Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel Withe novel acceptor splice site mutation 11396(G-->A) in the factor
                                                                                                                                                                                           Fujikawa K., McMullen B.A.;
"Amino acid sequence of hum
                                                                                                                                                                                                                                        MEDLINE=83291041; PubMed=6604055;
                                                                                                                                                                                                                                                                                                                                                                McMullen B.A., Fujikawa K.;
"Amino acid sequence of the heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85182674; PubMed=3886654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 25:1525-1528(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Que B.G., Davie E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86216049; PubMed=3011063;
                                                                        MEDLINE=96133302; PubMed=8528215;
                                                                                               TISSUE-Blood
                                                                                                                        SEQUENCE OF 561-615 FROM N.A.
                                                                                                                                                                     J. Biol.
                                                                                                                                                                                                                                                                    SEQUENCE OF 354-362 AND 373-615
                                                                                                                                                                                                                                                                                                                                       (activated Hageman factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 20-379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Characterization of
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  gene
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                                                                                                                                                                                                                                                                                                                   Chem. 260:5328-5341(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem.
     causes
                                                                                                                                                                          Chem. 258:10924-10933(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
factor XII precursor (EC 3.4.21.38) (Hageman factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262:13662-13673(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260:13666-13676(1985).
     a truncated transcript in cross-reacting
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a cDNA coding
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                                                                                                                                                                                                human beta-factor XIIa.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor XII (Hageman).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor XII cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor XII (Hageman
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          material
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RL J. BIOL. Chem. 267:5102-5107(1992).

RL J. BIOL. Chem. 267:5102-5107(1992).

CC -!- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE CC GENERATION OF BRADYKININ AND ANGIOTENSIN.

CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-1le bonds in factor CI to form factor VII a and factor XI to form factor XIA.

CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-1le bonds in factor CI to form factor XIA.

CC -!- PMM: O- AND N-GLYCOSYLATED.

CC -!- PMM: O- AND N-GLYCOSYLATED.

CC -!- PMM: O- AND N-GLYCOSYLATED.

CC -!- PMM: O- AND M-GLYCOSYLATED.

CC -!- PMM: O- AND M-GLYCOSYLATED.

CC -!- MISCELLANEOUS: FACTOR XII, PERCALLIKREIN, AND HMW KININGEN FORM A COMPLEX BOUND TO AN ANIONIC SURFACE, PREKALLIKREIN IS CLEAVED BY FACTOR XII AND THEN TO BETA-FACTOR XII FIRST COMPLEX BOUND TO AN ANIONIC SURFACE, PREKALLIKREIN IS CLEAVED BY FACTOR XII AND THEN TO BETA-FACTOR XII FIRST CONTAINS 2 EGF-LIKE DOMAIN.

CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPETN FAMILY
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000562; Fm_Type_II.
InterPro; IPR00001; Kringle.
InterPro; IPR001254; Trypsin.
InterPro; IPR00183; fibronectin_type_I.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; fn1; 1.
                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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the Euro
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MEDLINE-92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman M.W.;

"O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C.";

J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353-->Pro leading to loss of a kallikrein cleavage site."; Blood 84:1173-1181(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94325559; PubMed=8049433; Hovinga J.K., Schaller J., Stricker
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Laemmle B.;
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MI, M11723; AAA5198
ML; M17466; AAB5949
ML; M17464; AAB5949
ML; M17465; AAB5949
ML; M1747; AAB7022
M1; U71274; AAB5120
M1; A29411; KFHU12.
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                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long
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. Genet. 4:1235-1237(1995).
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AAA51986.1;
AAB59490.1;
AAB59490.1;
AAB59490.1;
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20
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Best Local
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PROSITE; PS00022; EGF_1; 2.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01253; FIBRONECTIN_1; 1.

PROSITE; PS00023; FIBRONECTIN_2; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS50070; KRINGLE_2; 1.
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PROSITE; PS01186; E
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Hydrolase; Fibrinolysis;
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SMART; SM00130; KR; 1.
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00013; FNTYPEII.
1 RNPDGDVGGPWAYTTNPRKL-YDY
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SM00058; FN1;
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                               Conservative
                                                                                               kringle;
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                                                                                              coagulation; Plasma; Kringle;
ysis; Signal; EGF-like domain;
                                           35.5%;
41.7%;
                              Score 49; DB
Pred. No. 15;
5; Mismatches
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O-LINKED (POTENTIAL).
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O-LINKED
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23
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BETA-FACTOR XIIA PART
FIBRONECTIN TYPE-II.
EGF-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH
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Repeat; Zymogen;
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Вb

267 RNPDNDI-RPWCFVLNRDRLSWEY

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PMA7
RESULT
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Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

Ra De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

Ra Wincker P., Cattolico L., Weissenbach J., Sandt P., Nyakatura G.,

Ra Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Ra Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D.,

Rocker R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

Ra Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

Rocker R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,

Ra Monfort A., Argiriou A., Flores M., Liquori R., Vitale D.,

Ra Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

Ra Mannhaupt G., Haase D., Schoof H., Studori R., Vitale D.,

Ra Mannhaupt G., Haase D., Schoof H., Studori R., Vitale D.,

Ra Mannhaupt G., Maiti R., Wu D., Peterson J., Van Aken S.,

Ra Pai G., Militscher J., Sallers P., Gill J.E., Feldblyum T.V.,

Ra Pai G., Militscher J., Sallers P., Gill J.E., Feldblyum T.V.,

Ra Ra Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

Ra Wincker R., Kaneko T., Kaneko T., Kaneko T.,

Ra Wincker R., Kaneko T., Kaneko T.,

Ra Wincker R., Kaneko T., Kan
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Arpase 7, plasma membrane-+
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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-i- FUNCTION: THE PLASMA MEMBRANE H+ ATPASE OF PLANTS AND FUNGI-
-i- EUNCTION: THE PLASMA MEMBRANE H+ ATPASE OF PLANTS AND FUNGI-
-i- EUNCTION AND FUNGINE THAT DRIVES THE ACTIVE TRANSPORT OF
NUTRIENTS BY H+-SYMPORT. THE RESULTING EXTERNAL ACTIVETION
AND/OR INTERNAL ALKINIZATION MAY MEDIATE GROWTH RESPONSES (BY
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                                              EMBL; AL163852; CAB87870.1;
                       InterPro;
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPA (E1-E2 ATPASES). SUBFAMILY IIIA.
                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: BINDS TO 14-3-3 PROTEINS. T
PHOSPHORYLATION OF THR-960. BINDING
THE H+-ATPASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(IN) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
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IPR004014;
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InterPro; IPR001454; HydroLase.
Pfam; PF00690; Cattion_ATPase_N;
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00154; ATPASE_E1_E2; 1.

Hvdrolase; Hydrogen ion transport; Transmembrane; Phosphorylation;
STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00119; CATATPASE. PRINTS; PR00120; HATPASE.
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
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                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MJ0145
                                                                                                                                                                                                                                                                                                                                                                                                                     Q57609;
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9; Conser
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97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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CYTOPLASMIC (POTENTIAL).
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7 (POTENTIA
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EXTRACELLULAR (POTENTIAL)
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PHOSPHORYLATION (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
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Best Local
                                                                                                                                                                                                                                                                                             MEDLINE—98295987; pubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C. E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                            STRAIN-CDC 1551 / Oshkosh;
FleisChmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                   P95245;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phospholipase C 3 precursor (EC 3.1.4.3).
PLCC OR RV2349C OR MT2414 OR MTCY98.18C.
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                               -!- SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C FAMILY.
                                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; SEQUENCE 268 AA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67471; AAB98128.1; TIGR; MJ0145; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                       PLCA/B/C
     SWISS-PROT entry is
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                                                       REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Complete proteome.
30285 MW; 627BBD523868B05B CRC64;
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57.1%;
     copyright.
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Pred. No.
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produced through a collaboration
                                                                   IN THE PHOSPHOLIPASE
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J. Virol
-!- MISC
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01-AUG-1992
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                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                   PRINTS; PR00939; C2HCZNFINGER PRINTS; PR00234; HIV1MATRIX.
                                                                                                                                                                                                      EMBL; M29975; AAA91905.1; -. HSSP; P03351; 1EIA.
            CHAIN
                                           AIDS;
                                                      PROSITE; PS50158; ZF_CCHC;
                                                                     SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                           InterPro; IPR000071;
InterPro; IPR001878;
                                                                                                                                                                                        InterPro; IPR000721;
                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson P.R., Fomsgaard A., Allan J., Gravell M., London W.T., Olmstead R.A., Hirsch V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90156504; PubMed=2304139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
entities requires a license agreement (See http://www.isb-sib.ch/an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyprotein [Contains: Core proteins P17, P24, and P15].
                                                                                                               PF00540; gag_p17;
PF00607; gag_p24;
PF00098; zf-CCHC;
                                           Core
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genetic diversity.";
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       protein; Polyprotein; Zinc-finger; Repeat.

1 141 CORE PROTEIN P17.

142 520 CORE PROTEINS P24 AND P1
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
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Retroviral_gag_p17.
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88.9%;
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SEQUENCE
                      P45880; Q9Y516;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)
                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                     HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Plasmid IncP-beta R751
                                                                                                                                                                                                                                                                                                    EMBL; X59794; CAA42459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Gene organization and nucleotide sequence of the primase region of IncP plasmids RP4 and R751.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-HB101
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             (Outer mitochondrial membrane
                                                                                      POR2_HUMAN
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Pred. No. 6.
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             protein porin
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EMBL;

193245;

InterPro;

IPR001925; Euk_porin.

AAD40241

EMBL; EMBL; EMBL;

Pfam; PF01459; E PRINTS; PR00185;

Euk_porin; 1. 5; EUKARYTPORIN

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Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Blachly-Dyson E., Zambronicz E.B., Yu W.H., Adams V., McCabe E.R.,
Adelman J., Colombini M., Forte M.;
"Cloning and functional expression in yeast of two human isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 270:13998-14006(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Decker W.K., Bowles K.R., Schatte E.C., Towbin J.A., Craige "Revised fine mapping of the human voltage-dependent anion loci by radiation hybrid analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 4).
MEDLINE=99431679; PubMed=10501981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93280191; PubMed=7685033;
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                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subcellular localization of human voltage-dependent anion channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Outer mitochondrial membrane ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), produced by alternative splicing and possibly alternative.
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS. SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: FORMS A CHANNEL THROUGH THE MITOCHONDRIAL OUTER MEMBRANE THAT ALLOWS DIFFUSION OF MALL HYDROPHILIC MOLECULES. THE CHANNEL ADDOPS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS ABOVE 30-40 M
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AF152227;
AF152220;
AF152221;
AF152222;
AF152223;
AF152224;
AF152225;
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                                                                                                                                                                             L08666; AAA60145.1;
L06328; AAB59457.1;
                                                                                                                                                                                                                        L08666; AAA60144.1;
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                    AAD40241.1;
AAD40241.1;
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Best Local
             ZN_FING
                                                             CHAIN
                                                                                                                                                      PRINTS; PRO0939; C2HCZNFINGER. PRINTS; PRO0234; HIV1MATRIX. SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                              Pfam; PF00540; gag_p17; Pfam; PF00607; gag_p24; Pfam; PF00098; zf-CCHC;
                                                                                                                                                                                                                                                                                      HSSP; P05888; lAAF.
HIV; X07805; GAG$AGMTY.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retroviral_gag_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-88232906; PubMed=3374586;
Fukasawa M., Miura T., Hassegawa A., Morikawa S., Tsujimoto H.,
Miki K., Kitamura T., Hayami M.;
"Sequence of simian immunodeficiency virus from African green monkey,
a new member of the HIV/SIV group.";
Nature 33:457-461(1988).
-!- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
!- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins p17, GAG.
                                                                                                           AIDS; Core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simian immunodeficiency virus (TYO-1 isolate) (SIY-AGM). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A30045; FOLJG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X07805; CAA30657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P05892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAG_SIVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative initiation; Polymorphism.

VARSPLIC 1 26 MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane; Porin; Mitochondrion; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 VGSPWSWRLNPAERNLWEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VGGPWAYTTNP--RKLYDY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rocat
                                          400343; ZECCHC; 2.
PS50158; ZECCHC; 2.
re protein; Polyprotein; Zinc-finger; Repeat.
CORE PROTEIN PL7.
CORE PROTEIN PL7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00558;
        142
397
418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
        141
519
414
435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTIC_PORIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
CCHC-TYPE 1.
CCHC-TYPE 2.
                                                CORE PROTEINS P24 AND P15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P (IN ISOFORM 3).
SPWSWRLNPAERNLWEWISEDLALIYFHCDQQQAFFPPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQNKG -> LALEEA (IN ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSWCNELRLPALKQHSIGRGLESHIT -> MATHGQTCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_006381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_006380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23F8ACA61184A1BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P24, and P15].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
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AC IJ

FA12_CAVPO Q04962;

STANDARD;

PRT;

603 AA

FA12_CAVPO

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RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
GAG_SIVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ъ
                                                                                                  Matches
                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                            ZN_FING
SEQUENCE
                                                                                                                                                                                                                                            PRINTS; PRO0939; C2HCZNFINGER.
PRINTS; PRO0234; HIV1MATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                       InterPro; IPR001878; Znf
Pfam; PF00540; gag_p17;
Pfam; PF000607; gag_p24;
Pfam; PF00098; zf-CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     African green monkeys: a novel type of intragroup divergence. Virology 176:216-221(1990).

-I- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.

-I- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000071; Retroviral_gag_p17.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M30931; AAA91913.1; -. HSSP; P03351; 1EIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                         ZN_FING
                                                                                                                                                                                                                                    AIDS; Core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
03-6AG polyprotein (Contains: Core proteins P17,
                                        241 RDPRGSDIAGTTSTVQEQLEWIYTANPR 268
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000721; Gag_p24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90232731; PubMed=2158689;
Baier M., Garber C., Mueller C., Cichutek K., Kurth R.;
"Complete nucleotide sequence of a simian immunodeficiency virus from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian immunodeficiency virus (AGM3 isolate) (SIV-AGM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P27978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAG_SIVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 RDPRGSDIAGTTSSVQEQLEWIYTANPR 264
                                                                    1 RNPDG-DVGG-----PWAYTTNPR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RNPDG-DVGG-----PWAYTTNPR 18
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                          402
423
521 AA;
                                                                                                                                                                                                                  protein; Polyprotein; Zinc-finger; Repeat.

1 145 CORE PROTEIN P17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 AA;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                      521
419
                                                                                                                                                                          440
                                                                                                                                                          58409 MW;
                                                                                                             33.3%;
                                                                                                                                                                                                                                                                                                                                                    Znf_CCHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58143 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                   CORE PROTEIN P17.
CORE PROTEINS P24 AND P15
CCHC-TYPE 1.
                                                                                                             Pred. No.
                                                                                                                           Score 46;
                                                                                                                                                                          CCHC-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                       1F111BD2F2EDF4F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85A3AC06BCCDCA38 CRC64;
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521
                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                           Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P24, and P15].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 519;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ņ
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Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Probom; PP000995; FN_Type_II; 1
SMART; SM00181; EGF; 2.
SMART; SM00089; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00120; Tryp_SPC; 1.
PROSITE; PS01022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01023; FIBRONECTIN_1
PROSITE; PS01023; FIBRONECTIN_2
PROSITE; PS00021; KRINGLE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996
01-FEB-1996
01-NOV-1997
Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primary structure of guinea-plq Hageman factor: sequence around the cleavage site differs from the human molecule."; Blochim. Blophys. Acta 1159:113-121(1992).

1- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE GENERATION OF BRADYKININ AND ANGIOTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                           InterPro;
Pfam; PF0
                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Semba U., Yamamoto T.
Kambara T., Okabe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93003367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Cleaves selectively Arg-[-Ile bonds in factor VII to form factor VIIa and factor XI to form factor XIa.

VII to form factor VIIa and factor XI to form factor XIa.

MISCELLANEOUS: FACTOR XII, PREKALLIKERIN, AND HMW KININOGEN FORM A COMPDEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BY FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XII FIRST TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR XIA ACTIVATES FACTOR XI TO FACTOR XIA.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TREVESTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY.
                                                                                                                                                                                                                                       ; PF00040;
; PF00051;
; PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
                                                                                                                                                                                                                                                                                             PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X68615;
SW00020; Tryp_SPc; 1.

SW00022; EGF_1; 2.

SPS01186; EGF_2; 1.

PS01186; EGF_2; 1.

PS01233; FIBRONECTIN_1; 1.

PS00023; FIBRONECTIN_2; 1.

PS00021; KRINGLE_1; 1.

PS500021; KRINGLE_2; 1.

PS500701; KRINGLE_2; 1.

PS500701; FRYPSIN_DOM; 1.

PS50240; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                         IPR000562; I
IPR000001; E
IPR001254; 7
                                                                                                                                                                                                                                                                                                                                                                                           IPR000742;
IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 35, Last annotation updat
factor XII precursor (EC 3.4.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1RTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA48600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1390917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, Last annotation update)
XII precursor (EC 3.4.21.38) (Hageman factor)
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                                                                                                                                                                                                                                                                                                                                                             EGF-like.
EGF_2.
EGF_Ca.
FN_Type_II.
Kringle.
                                                                                                                                                                                                                                                                                                                             Trypsin.
fibronectin_type_1
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Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibuya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318-332 AND 359-373
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L. Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R., Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00135;
                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 42.4 kDa protein in CTR2-STB5 intergenic region.
YHR176W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                              STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     YHX6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PDGDVGGPWAYTTNPRKLYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                 |: | || || |:|: |:
|PNFDQDQQWAYCLEPKKVKDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrinolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135; TRYPSIN_SER; 1. Blood coagulation;
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                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation; Plasma; Kringle;
ysis; EGF-like domain; Repeat;
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38.1%;
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ALPHA-FACTOR XIIA LI
FIBRONECTIN TYPE-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 39;
4; Mismatches
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Y SYSTEM
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(BY
YB)
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RESULT 47
OASL_HUMAN
ID 0.15646
DT 01.NOV
DT 30.AMAY
DT 16-OCT
DE 59 kDa
DE (9590A
GN OASL 0
OS HOMO S
OC EUKARY
OC Mammal
OX NCBL_T
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RP SEQUEN
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                                SEQUENCE OF 260-416 FROM N.A. (ISOFORM P56).
MEDLINE-95295737; PubMed-7776974;
Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.;
"Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OASI_HUMAN STANDARD; PRT; 514 AA.

015646; 075686; Q9Y6K7; Q9Y6K6;

01.NOV-1997 (Rel. 35, Created)

30-NAY-2000 (Rel. 39, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

59 kDa 2'-5'-oligoadenylate synthetase like protein (p59 OASL)

(p59OASL) (Thyroid receptor interacting protein 14) (TRIP14).

OASL OR TRIP14.
                                                                                                                                                                                                                                                              Rebouillat D., Marie I., Hovanessian A.G.;
"Molecular cloning and characterization of two related and interferon-
induced 56-kDa and 30-kDa proteins highly similar to 2'-5'
oligoadenylate synthetase."
                                                                                                                                                              Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Monocytes;
MEDLINE=99041549; PubMed=9826176;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS P56 AND P30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartmann R., Olsen H.S., Widder S., Joergensen R., Justesen J.; "p590ASL, a 2'-5' oligoadenylate synthetase like protein: a novel human gene related to the 2'-5' oligoadenylate synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM P56).
MEDLINE=98391734; PubMed=9722630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000960; FMO.
Pfam; PF00743; FMO-like; 1.
PRINTS; PR00370; FMOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U00027; AAB68021.1; -. PIR; S48915; S48915. SGD; S0001219; YHR176W.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 26:4121-4127(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Oxidoreductase; Flavoprotein; FAD. SEQUENCE 373 AA; 42440 MW; DFB5BAll956896CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome \mathtt{VIII.} ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 265:2077-2082(1994)
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    Endocrinol.
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9; Conserv
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9:243-254(1995)
                                                                                                                                                                                                                                                     257:319-330(1998)
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Pred. No. 2
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                                                                                                                  SEQUENCE
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                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMOUZI, ..., 25A_SYNTH_1; 1.
PROSITE; PS00833; 25A_SYNTH_2; 1.
PROSITE; PS00833; 25A_SYNTH_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50152; 25A_SYNTH_3; PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00240; ubiquitin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ225089; CAA12396.1; -.
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439 KNPD---GGSYAYAINP 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001797; InterPro; IPR001201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 603281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                      Local
                          1 RNPDGDVGGPWAYTTNP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DOES NOT HAVE 2'-5'-OAS ACTIVITY, BUT BINDS DOUBLE-
STRANDED RNA AND DNA.

STRANDED RNA AND DNA AND PRESENCE OF THYROID HORMONE FOR ITS INTERRACTION.

ALTERNATIVE PRODUCTS: 2 ISOPORMS; P56 (SHOWN HERE) AND P30; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

TISSUES SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH THE HIGHEST LEVELS IN PRIMARY BLOOD LEUKOCYTES AND OTHER HEMATOPOIETIC SYSTEM TISSUES, COLON, STOMACH AND TO SOME EXTENT IN TESTIS.

INDUCTION: BY INTERFERONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY. SIMILARITY: CONTAINS 2 UBIQUITIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF063611; AAD28541.1; -.
AF063612; AAD28542.1; -.
Z93097; -; NOT_ANNOTATED_CDS.
L40387; AAG41733.1; ALT_FRAME.
P022248; 1UBI.
                                                       Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000626;
                                                                                                                514 AA;
                                                                                                                                                                                                                                                                                                                                     354
434
220
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                     Interferon
354 433
434 509
220 255
                                                                                                                                                                                                                                                                             256
26
                                                                                                                                                                                                                                    95
                                                                                                                                            223
317
321
324
342
                                                                                                               59226
                                                                   33.0%;
52.9%;
                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25A_synth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAP_25A_core
                                                                                                                                                                                                                                                                                                                                                                           induction; Alternative splicing; Repeat
                                                                                                                                                    QEAAKHKDVLRLIWKTMW -> P
V (IN REF. 2).
A -> S (IN REF. 2).
Y -> I (IN REF. 2).
I -> T (IN REF. 2).
Q -> L (IN REF. 2).
                                                     2;
                                                                  Score 45.5;
Pred. No. 39
                                                                                                             NP -> KG (IN REF. 4).
S -> T (IN REF. 2; AAD28541).
; 4D8BB655D9EA003E CRC64;
                                                                                                                                                                                                                                                                                          ISOFORM P30).
MISSING (IN ISOFORM P30)
                                                                                                                                                                                                                                                S -> T (IN REF.
                                                                                                                                                                                                                                                                            HREWKEEVLDAVR
                                                                                                                                                                                                                                                                                                                                                   UBIQUITIN-LIKE 1. UBIQUITIN-LIKE 2.
                                                                                                                                                                                                                                                                                                                    HHPGSGRPHPQRGRRVQMGHRCSEGLPVPETGLLL
                                                                                                                                                                                                                                                                                                                                  YVKARSPRANLPPLYALELLTIYAWEMGTEEDENFM ->
                                                    Mismatches
                                                                                 DB
                                                                                                                                                                                                                                                                             Ÿ
                                                                                1; Length 514;
                                                                                                                                                                                                                                              2; AAD28542)
                                                                                                                                                                                                                                                                            TGVEGRGARRCA (IN REF
                                                                                                                                                                                                                                 PGGSQASQRCSEADMENH
                                                    ω,.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                     (IN
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PPO_VITVI
ID PPO_VITVI

STANDARD;

607

RESULT 48

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RESULT
RETR_MC
ID NETR_MC
ID OC
AC OC
DT 30
DT 30
DT 16
DT 1
                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                   008762;
30-MAY-2000
30-MAY-2000
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95036022; PubMed-7948897;
Dry I.B., Robinson S D .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43311;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. 26:495-502(1994).
-!- FUNCTION: CATALYZE THE OXIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vitis vinifera (Grape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyphenol oxidase, chloroplast precursor (EC (Catechol oxidase)
                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Neurotrypsin precursor (EC 3.4.21.-) (Motop
protease 3) (BSSP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00264; tyrosinase; 1. PRINTS; PR00092; TYROSINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z27411;
EMBL; A27657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and characterisation
    Eukaryota;
                        Mus musculus
                                                                                                                                                                                                                  NETR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                   PRSS12 OR BSSP3
                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                               2 NPDGDVGGPWAYTTNPRKLYD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for contents are not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: 2 catechol + O(2) = 2 1,2-benzoquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                     NPDG-MYMPTIYASSPSSLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00497; TYROSINASE_1; 1.
PS00498; TYROSINASE_2; 1.
luctase; Copper; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411; CAA81798.1; -.
657; CAA01887.1; -.
IPR002227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDS TWO COPPER IONS (BY SIMILARITY)
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67347
       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast;
                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPHENOL OXIDASE.
COPPER A (BY SIMILAR
COPPER B (BY SIMILAR
COPPER B (BY SIMILAR
COPPER B (BY SIMILAR
COPPER B (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -binding; Chloroplast; T
CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                    PRT;
       Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B9045598E69BC57B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A (BY SIMILARITY).
A (BY SIMILARITY).
B (BY SIMILARITY).
B (BY SIMILARITY).
B (BY SIMILARITY).
                                                                                               (Motopsin)
                                                                                                                                                                                                                    761
                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               within
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of grape berry
       Vertebrata;
                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.10.3.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the thylakoid lumen.
                                                                                               (Brain-specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-DIPHENOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transit
       Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyphenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PPO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    way
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THE THE TERM DESCRIPTION OF TH
                                                                                                                                                                                                                       PROSITE; PS50287; 9
PROSITE; PS50240; 9
PROSITE; PS00134; 9
PROSITE; PS00135; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97401523; PubMed=9245503;
Gschwend T.P., Krueger S.R., Kozlov S.V.,
"Neurotrypsin, a novel multidomain serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheri
NCBI_TaxID=10090;
DOMAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00051; kringle; 1. Pfam; PF00530; SRCR; 3. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1100881; Prss12.
InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO00001; Kringle.
InterPro; IPR001190; SRCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motifs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kringle-like structure and three scavenger receptor cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98008848; PubMed=9344839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous
                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                         PROSITE; PS00021;
PROSITE; PS50070;
PROSITE; PS00420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a novel brain-specific serine protease with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamura Y., Yamashiro K.,
                                                                                                                                                                              Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13192; CAA73646.1;
                                                                                         DOMAIN
                                                                                                           DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.237; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. Biophys. Res. Commun. 239:386-392(1997).
FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTION MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell. Neurosci. 9:207-219(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : D89871; BAA23986.1; -. P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system.":
                                                                                                                                                                                                                                                                                                                                                                              SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00722;
PR00018;
PR00258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMYGDALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                     Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND MEMORY OPERATIONS.
                                                                                                                                                                                                                                                                                                                                ; Tryp_SPc; 1.
21; KRINGLE_1;
70; KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              KRINGLE; FALSE_NEG. SPERACTRCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHYMOTRYPSIN
  protease;
21
761
157
267
373
373
487
761
516
                                                                                                                                                                                                                       TRYPSIN_HIS;
TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                              SRCR_1;
                                                                                                                                                                                                                                                                  TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                         SRCR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \omega \mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRCR DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuruoka N., Nakazato
                    SRCR 1.
SRCR 2.
SRCR 3.
SEXINE PROTEASE.
ZYMOGEN ACTIVATION REGION.
                                                                                                                                                                                                  Glycoprotein; Kringle;
                                                                                                                                  NEUROTRYPSIN.
KRINGLE.
                                                                                                                                                                                                                                                                                                                                                            FALSE_NEG
    REACTIVE BOND (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIPPOCAMPUS
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RESULT 50
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                                                                           EMBL; Z49702; CAA89750.1; -.

HSSP; P15925; 1FGS.

SGD; S0004719; FOL3.

InterPro; IPR001645; FOLYLPOLYGLU_SYNT.

Pfam; PF01225; Mur_ligase; 1.

PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1.

PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1.

PROSITE; PS01012; FOLYLPOLYGLU_SYNT_1; 1.

PROSITE; PS01012; FOLYLPOLYGLU_SYNT_1; 1.
 Query Match 32.6%;
Best Local Similarity 37.5%;
Matches 6; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOLD_YEAST STANDARD; PRT; 427 AA.
012676;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Folylpolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate
                                                                                                                                                                                                                                                                                                                                                                       Cherest H., Thomas D., Surdin-Kerjan Y.;

"Polyglutamylation of folate coenzymes is necessary for methionine biosynthesis and maintenance of intact mitochondrial genome in Saccharomyces cerevisiae.";

J. Biol. Chem. 275:14056-14063(2000).

I. FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.

I. CATALYTIC ACTIVITY: ATP + {tetrahydrofolyl-[Glu]}(N) + L-glutamate = ADP + phosphate + {tetrahydrofolyl-[Glu]}(N+1).

I. SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE=20261521; PubMed=10799479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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FOL3 OR YMR113W OR YM9718.12.
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9; Conservative
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761 AA;
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39.1%;
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   5; Mismatches
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                  Score 45; DB 1; Length 427; Pred. No. 38;
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N-LINKED (
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).;
DF507B03712164E6 CRC64;
                                                                C3307CEF43BE1F30 CRC64;
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RELAY SYSTEM.
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Qy 8 GGPWAYTTNPRKLYDY 23
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Db 356 GMPWIHATDPEEIKDF 371
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Search completed: November 8, 2002, 09:31:41 Job time : 12 secs

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